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(71) Applicant: SENOMYX, INC. [US/US]; Suite 160, 11099
N. Torrey Pines Road, La Jolla, CA 92037 (US).

(72) Inventors: ZOZULYA, Sergey; 3950 Mahaila Avenue
#B22, San Diego, CA 92122 (US). STRYER, Lubert; c/o
Senomyx, Inc., 11099 N. Torrey Pines Road, Suite 160, La
Jolla, CA 92037 (US).

(74) Agents: TESKIN, Robin, L. et al.; Pillsbury Winthrop
LLP, 1600 Tysons Boulevard, McLean, VA 22102 (US).

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(54) Title: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

(57) Abstract: The use of sensory G protein-coupled receptors that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants is described. The use of such products as a biosensor or a components thereof to detect, identify, measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant) is also described. The invention has application, for example, in the design and formulation of odorant and tastant compositions.

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RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

Cross Reference to Related Application

This application is related to U.S. Provisional Serial No. 60/213,812, filed June 22, 2000, and U.S. Serial No. 09/804,291, filed March 13, 2001, which are incorporated by reference in their entirety.

Background of the Invention

Field of the Invention

The invention relates to the use of sensory G protein-coupled receptor complexes that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants. The invention also relates to the use of such products as a biosensor or component thereof to detect, to identify, to measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant). The invention has application, for example, in the design and formulation of odorant and tastant compositions.

25 Description of the Related Art

The olfactory and taste systems provide sensory information about the chemical environment. Olfactory receptors and taste receptors recognize, respectively, "odorants" and "tastants," collectively referred to as "sensants" or "sensory receptor ligands" herein. A "primary" sensant is an odorant or tastant ligand that substantially binds to sensory receptors with a ligand-binding site of a single amino acid sequence. Olfactory and taste receptors belong to the superfamily of seven-transmembrane guanyl nucleotide-binding proteins: such receptors are, however, also recognized as distinct families, or sub-genuses, of olfactory or taste

receptors (see Raming *Nature* 361:353, 1993). These receptors control diverse physiological functions such as media-ting signaling from an external chemical stimulus across the membrane containing the receptor into a cell, endocrine function, exocrine function, heart rate, lipolysis, and carbohydrate metabolism. Thus, the
5 dissection of these diverse functions into component signals is needed.

But the complexities of sensory perception of chemical sensants prevent easy translation of the olfaction and taste systems to a machine sensor. For example, U.S. Patent Nos. 5,675,070; 5,918,257; 5,928,609; and 6,085,576 disclose machine sensors that use various chemistries, but they do not take advantage of the specificity of
10 olfactory and taste receptors for their cognate ligands to produce a biosensor.

WO 00/15269 discloses methods and apparatus for odor reproduction. The total affinities of a specific odorant with a group of receptors was called the affinity fingerprint of the odorant. This odorant fingerprint was represented by a vector of affinity values. It was proposed to repro-duce an arbitrary odor by inputting its sensed
15 odorant fingerprint into a device, which has a palate of predetermined odorants and produces a composite odor using predetermined odorant finger-prints by minimizing the difference between vectors representing the sensed odorant fingerprint and the predetermined odorant fingerprints. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

WO 00/70343 discloses biosensors and sense replication systems using G-protein coupled receptors (GPCR). It was proposed to mimic the response of the G-protein signal transduction system by detecting the affinity of a stimulus to a plurality of GPCR, codifying such information into electronic signals, and reproducing the stimulus by converting the codified information into a combination of stimulant
25 entities. But this reference also does not teach or suggest the human olfactory receptors disclosed herein.

WO 01/27158 discloses olfactory receptors and their use to determine the correspondence between individual odorant receptors and particular odors. It was proposed that the interactions between an odor and olfactory receptors can be used to
30 represent the odor and to re-create it. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

Dissecting the function of sensory receptors by binding sensory receptors of a clone of cells expressing a single sensory receptor gene, fragmentation of sensory

receptors to provide ligand-binding or signal-transducing domains thereof, and construction of fusion sensory receptor proteins will separate the diverse physiological functions associated with sensory perception at the level of ligand-receptor binding. Furthermore, novel "primary sensants" that are identified and isolated by the methods described herein may be used to further define the function of the cognate sensory receptor by uniquely enhancing or, in the alternative, blocking stimulation of sensory receptors with a single ligand-binding domain.

The present invention addresses the need for better understanding of these ligand-receptor interactions by using a large set of identified sensory receptors. Even if the receptor set used is incomplete (*i.e.*, a partial set of all sensory receptors encoded in the genome), a large number of sensants will be detected. Moreover, redundancy in the chemical structures recognized by the sensory receptors or combinatorial processing of signals from different sensory receptors would allow broad coverage of chemically diverse sensants (*e.g.*, by selection of a representative class of sensory receptors). Also provided are, *inter alia*, methods for utilizing such sensory receptors and biosensors to simulate sensory perception. To analyze ligand-receptor interactions and their effects on cell signaling and the processing of those signals in sensory perception, specific sensants and their cognate receptor complexes are detected, identified, and measured under binding conditions. Fragrances and flavorings can be detected, identified, measured, and/or custom designed by the methods herein described. In addition, drugs that incorporate artificial odors and/or tastes can be formulated.

Summary of the Invention

Large gene families encoding mammalian olfactory G-protein-coupled receptors (OLFR) and mammalian taste G-protein-coupled receptors (TASR) are known in the prior art or are disclosed herein. An object of the invention to provide fragments and variants of such OLFRs and TASRs which retain odorant- or tastant-binding activity, respectively. The large number of sensory receptors that are made available herein and now amenable to manipulation raises the confidence that a substantially complete, or at least functional, repertoire of sensory receptors is provided.

It is an object of the invention to provide nucleic acid sequences or molecules that encode such sensory receptors, or fragments or variants thereof. Another object is to provide expression vectors which include nucleic acid sequences that encode such sensory receptors, or fragments or variants thereof. It is yet another object of the invention to provide human or non-human cells which functionally express at least one of such sensory receptors, or fragments or variants thereof. Still another object is to provide sensory receptor fusion proteins or other polypeptides which include at least a fragment of at least one of such sensory receptors. In particular, fusions with reporter molecules or other heterologous amino acid sequences may maintain the original ligand-properties while changing the signaling properties to allow easier detection of sensant binding to the receptor (*e.g.*, change in fluorescent signal). Moreover, chimeric proteins or other polypeptides with altered ligand-binding and/or signaling properties can be made from two or more different sensory receptors by mixing domains.

15 The invention provides methods for representing the sensory perception of one or more chemicals (*e.g.*, a primary sensant or mixture thereof) and/or for predicting the sensory perception of one or more chemicals in a mammal (*e.g.*, human) using the aforementioned products. Given a known member of a ligand-receptor binding pair, one or both members of the pair (*i.e.*, ligand, receptor, or both) may be detected, identified, and/or measured under binding conditions.

20 Novel molecules or combinations of molecules which elicit a desired and predetermined sensory perception in a mammal (*e.g.*, human) can be generated by determining a value of sensory perception in a mammal for a known molecule or combination thereof; determining a value of sensory perception in a mammal for one or more unknown molecules or combinations thereof; comparing the value of sensory perception in a mammal for one or more unknown compositions to the value of sensory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined sensory perception in a mammal; and mixing two or more unknown molecules or combinations thereof to form a molecule or combination thereof that elicits a predetermined sensory perception in a mammal. The combining step yields a single molecule or a combination thereof that elicits a predetermined sensory perception in a mammal. In particular, primary odorants that uniquely bind to olfactory receptors with a single

ligand-binding domain may be such novel molecules. Variants thereof may be used (1) to enhance stimulation of a limited response by olfactory receptors with a single ligand-binding domain or (2) to block stimulation of olfactory receptors with a single ligand-binding domain to reduce or inhibit olfactory perception. An alternative method for identifying primary odorants is to identify the mutated receptors in genetic anosmias because that odorant would be expected to be recognized by only one or a few olfactory receptors affected by the mutation.

Detailed Description of the Invention

10 Perception of Chemical Sensants

U.S. Patent No. 5,691,188 describes how upon binding of ligand to receptor, the receptor presumably undergoes a conformational change leading to activation of the G protein. The G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of disso-ciation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell. A high-resolution X-ray crystal structure is available for rhodopsin, a guanyl nucleotide binding protein, has been solved (Palczewski *et al.*, *Science* 289:739, 2000). Using this structure, the portions of the amino acid sequence of sensant receptors that are responsible for ligand binding can be identified.

30

Sensory Perception - Olfaction

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel *Sci. Amer.* 273:154, 1995). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer *Semin. Cell Biol.* 5:25, 1994). The human genome contains thousands of genes that encode a diverse repertoire of olfactory receptors (Rouquier *Nat. Genet.* 18:243, 1998; Trask *Hum. Mol. Genet.* 7:2007, 1998). An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that sensory receptors belong to a multigene family with over a thousand members, and the odorant receptors number at least 500 to 1,000. Moreover, each sensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses.

Sensory Perception - Taste

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). See, e.g., Kawamura *et al.*, *Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al.*, *Ann. Rev. Physiol.*, 54:715, 1992; Lindemann, *Physiol. Rev.*, 76:718, 1996; Stewart *et al.*, *Am. J. Physiol.*, 272:1, 1997. Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. See, e.g., Akabas *et al.*, *Science*, 242:1047, 1988; Gilbertson *et al.*, *J. Gen. Physiol.*, 100:803, 1992; Bernhardt *et al.*, *J. Physiol.*, 490:325, 1996; Cummings *et al.*, *J. Neurophysiol.*, 75:1256, 1996.

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds, e.g., mice, to thousands, e.g., human, of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, only contain dozens to hundreds of taste buds. Moreover, fungiform papillae contain only a single or a few taste buds, and are at the front of the tongue.

AC010814, AC018700, AC021304, AC008620, AC011537, AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, 5 AP001803, AP001804, AL353767, AP001884, AC026083, AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, 10 AP002826, AL359636, AL391534, AC055731, AC076959, AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes. Similarly, genes encoding five and thirty-six (36) distinct, novel human T1R and T2R taste receptors, respectively, have been identified in genome 15 sequence databases.

Alternatively, nucleic acids encoding the sensory receptors and other related polypeptides can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/35374, which is herein incorporated by reference in its entirety.

20 These nucleic acids provide probes for the identification of cells expressing sensory receptors, as the nucleic acids are specifically expressed in such cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between cells expressing sensory receptors and sensory neurons leading to particular regions of the brain. Furthermore, the nucleic acids and the 25 polypeptides they encode can be used as probes to elucidate olfactant- or tastant-induced behaviors.

Nucleic acid molecules encoding a sensory receptor comprising a nucleic acid sequence that is at least 75%, 85%, 90%, 95%, or 99% identical to a nucleic acid sequence selected from those known in the prior art or disclosed herein are considered 30 variants. Other nucleic acid molecules comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 75%, 85%, 90%, 95%, or 99% identical to an amino acid sequence selected from those known in the prior art or disclosed herein are also considered variants. Further variants contain amino acid

sequence differences in at most ten, five, four, three, two, or one amino acid residue(s).

Exemplary nucleic acid sequences may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

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 25 NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,
 SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512.

Nucleic acid molecule comprising a nucleic acid sequence that encodes a
 fragment of a polypeptide having an amino acid sequence selected from those known
 in the prior art or disclosed herein; wherein the fragment is at least ten, 20, 30, 50, 70,
 30 100, or 150 amino acid residues in length, are useful as probes, primers, and to
 construct hybrids or chimerae.

Polypeptides comprising an amino acid sequence that is at least 90%, 95%,
 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from those

known in the prior art or disclosed herein are considered variants. Further variants contain amino acid sequence differences in at most ten, five, four, three, two, or one amino acid residue(s). Other polypeptides comprising a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed
 5 herein; wherein the fragment is at least 40, 60, 80, 100, 150, 200, or 250 amino acid residues in length, are useful as specific binders of sensants, competitive binders, antigens, and to construct hybrids or chimerae.

Exemplary amino acid sequences may be selected from the group consisting of
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15 SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID
NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
20 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
25 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
30 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Also provided are methods of screening for modulators, *e.g.*, activators,
inhibitors, stimu-lators, enhancers, agonists, and antagonists, of the sensory receptors,

or fragments or variants thereof. Such modulators of signal transduction are useful for pharmacological or genetic modulation of signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of sensory cell activity. These modulator compounds can then be used in the pharmaceutical, food, and cosmetic industries to customize odorants or tastants.

Thus, the invention provides assays for sensory modulation, where the sensory receptors, or fragments or variants thereof, act as direct or indirect reporter molecules for the effect of modulators on signal transduction. Sensory receptors, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, sensory receptors, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g., Mistili et al., Nature Biotech., 15:961, 1997*). In another embodiment, the sensory receptors, or fragments or variants thereof, can be expressed in host cells, and modulation of signal transduction via sensory receptor activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of signal transduction include *in vitro* ligand binding assays using the sensory receptors, or fragments or variants thereof. More particularly, such assays can use the sensory receptors; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G-protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting sensory receptor nucleic acid and protein expression, allowing for the investigation of taste transduction regulation and specific identification of sensory receptor cells. The sensory receptors, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying a sensory receptor cells. Sensory receptor cells can be identified using techniques such as reverse transcription and amplification

of mRNA, isolation of total RNA or poly A⁺ RNA, Northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, Western blots, and the like.

A. Identification and Characterization of Sensory Receptors

5 The amino acid sequences of the sensory receptors and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

10 For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as
15 described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

 A "comparison window," as used herein, includes reference to a segment of
20 any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment
25 of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and
30 TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J Mol. Biol.* 215:403, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (see, e.g., Figure 2). PILEUP uses a simplification of the progressive

alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351, 1987. The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151, 1989. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7.0 (Devereaux *et al.*, *Nucl. Acids Res.* 12:387, 1984) encoded by the genes were derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the olfactory receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative sensory receptor proteins generally having lengths of about 300 to about 400 amino acid residues that contain seven transmembrane domains, as predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the 256 sensory receptors identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all 256 sequences contain very close matches to the following consensus amino acid motifs (Mombaerts, 1999; Pilpel, 1999): LHTPMY in intracellular loop 1, MAYDRYVAIC at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5,

FSTCSSH in the beginning of transmembrane domain 6, and PMLNPF in transmembrane domain 7. Combination of all the above mentioned structural features of the 256 genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

5 As noted above, complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human sensory receptors, which suggests their different specificity in sensant recognition. Therefore, these novel sensory receptors and their genes can be used, alone or in combination
10 with known sensory receptors, in developing detection systems and assays for chemically distinct types of sensants not recognized by the known sensory receptors, as well as for diagnostic and research purposes.

B. Definitions

The terms "purified," "substantially purified," and "isolated" as used herein
15 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
20 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
25 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or
30 proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

The terms “amplifying” and “amplification” refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, sensant-binding sequences of the invention) *in vivo* or *in vitro*.

The term “7- transmembrane receptor” means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma membrane seven times (thus, the seven domains are called “transmembrane” or “TM” domains TM I to TM VII). The families of olfactory and taste receptors each belong to this super-family. Seven-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

The term “expression vector” refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression “cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

The term “library” means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated sensory, particularly olfactory or taste, receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of vectors that incorporate the amplified sensant-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding a sensory receptor.

The term “nucleic acid” or “nucleic acid sequence” refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, *i.e.*, oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like

structures with synthetic backbones, *see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Anti-sense Strategies*, Annals of the N.Y. Academy of Sciences, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156.

The term sensory receptor "ligand-binding region" refers to sequences derived from a sensory receptor that substantially incorporates transmembrane domains II to VII (TM II to VII). The domain may be capable of binding a sensant.

The terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the poly-peptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing function-ally similar amino acids are well known in the art.

For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): Ala/Gly or Ser; Arg/Lys; Asn/Gln or His; Asp/Glu; Cys/Ser; Gln/Asn; Gly/Asp; Gly/Ala or Pro; His/Asn or Gln; Ile/Leu or Val; Leu/Ile or val; Lys/Arg or Gln or Glu; Met/Leu or Tyr or Ile; Phe/Met or Leu or Tyr; Ser/Thr; Thr/Ser; Trp/Tyr; Tyr/Trp or Phe; Val/Ile or Leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman, 1984; Schultz & Schimer, *Principles of Protein Structure*, Springer-Verlag, 1979). One of skill in the art will appreciate that the above-identified substitutions are not the only possible

conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains or sensant-binding domains or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (see, *e.g.*, Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications,"

Marcell Dekker, NY). A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

As used herein, "recombinant" refers to a polynucleotide synthesized or
5 otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of
10 nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The term "transmembrane domain" means a polypeptide domain that can completely span the plasma membrane. The general secondary and tertiary structure
15 of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below.

C. Isolation and Expression of Olfactory Receptors

20 Isolation and expression of the sensory receptors, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional
25 expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or
30 decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can
5 be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983);
10 Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the
15 strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.
20 See, *e.g.*, Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation*, Tijssen, ed. Elsevier, N.Y. (1993).

25 Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, *e.g.*, analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion
30 chromatography, various immunological methods, *e.g.*, fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), immunofluorescent assay, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (*e.g.*, SDS-PAGE),

RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned
5 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, *e.g.*, polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis. Academic Press, NY, 1990
10 and *PCR Strategies*, ed. Innis, Academic Press, NY, 1995), ligase chain reaction (LCR) (*see, e.g.*, Wu, *Genomics* 4:560, 1989; Landegren, *Science* 241:1077, 1988; Barringer, *Gene* 89:117, 1990); transcription amplification (*see, e.g.*, Kwok, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989); and, self-sustained sequence replication (*see, e.g.*, Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990); Q Beta replicase
15 amplification (*see, e.g.*, Smith, *J. Clin. Microbiol.* 35:1477, 1997); automated Q-beta replicase amplification assay (*see, e.g.*, Burg, *Mol. Cell. Probes* 10:257, 1996) and other RNA polymerase mediated techniques (*e.g.*, NASBA, Cingene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307, 1987; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563, 1995.

20 Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Patent No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR
25 primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the sensant-binding region-coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be
30 translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted sensant-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I

and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify sensant-binding regions of olfactory receptor proteins. These domain regions may vary for different sensants, and more particularly odorants; thus, what may be a minimal binding region for one sensant, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane sensory receptor.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3'). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify a transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL, encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CA-NGT-3'. Such a degenerate primer can
 5 be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and
 10 is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucl. Acids Res.* 26:1628, 1998; Singh, *Biotechniques* 24:318, 1998).

Means to synthesize oligonucleotide primer pairs are well known in the art.
 15 "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition.
 20 Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866, 1997. Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950, 1998). For example, two degenerate bases can
 25 be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, Proc. Natl. Acad. Sci. USA* 95:4258, 1998). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, see
 30 above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.

Nucleic acids that encode ligand-binding regions of olfactory receptors are generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova, *Proc. Natl. Acad. Sci. USA* 93:9858, 1996). Shirley, *Eur. J. Biochem.* 32:485, 1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211, 1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*,

antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260, 1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

5 Hybrid protein-coding sequences comprising nucleic acids sensory receptors fused to the translocation sequences described herein may be constructed. Also provided are hybrid receptors comprising the translocation motifs and ligand-binding domains of sensory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, *e.g.*, transcription and translation
10 initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can
15 also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227, 1998). Receptor genes are normally expressed in a small subset of
20 neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

 Fusion proteins, either having C-terminal or, more preferably, N-terminal
25 translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized
30 metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289, 1998), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615, 1997); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane
5 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a nucleic acid sequence encoding a polypeptide linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787, 1995), and an amino terminal translocation domain. The histidine residues facilitate detection and
10 purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g., Kroll, DNA Cell. Biol.* 12:441, 1993).

Expression vectors, either as individual expression vectors or as libraries of
15 expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g., Roberts, Nature* 328:731, 1987; Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10, 1995; Sambrook; Tijssen; Ausubel. Product information from
20 manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses
25 which are stably or transiently expressed in cells (*e.g., episomal expression systems*). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic
30 resistance (*e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin*) or herbicide resistance (*e.g., chlorosulfuron or Basta*) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g., Blondelet-Rouault, Gene* 190:315, 1997; Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992, 1997). Because

selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a sensant-binding domain
5 within any 7-transmembrane polypeptide. Seven-transmembrane receptors belong to a superfamily of trans-membrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-trans-membrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains
10 (*e.g.*, TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To
15 predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969, 1999; Rost, *Protein Sci.* 4:521, 1995. Periodicity detection enhancement and alpha helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch,
20 *Receptors Channels* 4:161, 1996; Cronet, *Protein Eng.* 6:59, (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from-mRNA of or cDNA derived
25 from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of sensory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the
30 seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel *supra*), as described above. Using this information sequences flanking the seven

domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of, for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the sensory receptors described herein, coupled to additional amino acids representing all or part of another G protein receptor, preferably a member of the 7-transmembrane superfamily. These chimerae can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the 7-transmembrane protein described herein, and the remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous CGPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, e.g., green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a sensory receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to isolate sensory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a sensory receptor-derived polypeptide, which also recognize and selectively bind to the sensory receptor homolog.

Also within the scope of the invention are host cells for expressing the sensory receptors, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the sensory receptors, fragments, or variants thereof, the nucleic acid sequence of interest is subcloned into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable prokaryotic and eukaryotic expression systems are well known in the art and described, e.g., in Sambrook *et al.*

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Sambrook *et al.*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.,* WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of Sensory Receptor Polypeptides

In addition to the detection of sensory receptor genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect

sensory receptors, *e.g.*, to identify olfactory receptor cells, and variants of sensory receptor family members. Immunoassays can be used to qualitatively or quantitatively analyze the sensory receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

5 1. Antibodies to sensory receptor family members

 Methods of producing polyclonal and monoclonal antibodies that react specifically with a sensory receptor family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology*, 1991; Goding, *Monoclonal Antibodies: Principles and Practice*, 2d ed., 1986; Harlow & Lane, *supra*; and Kohler & Milstein, *Nature*, 256:495, 1975). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science*, 246:1275, 1989; Ward *et al.*, *Nature*, 341:544, 1989).

15 A number of sensory receptor-comprising immunogens may be used to produce antibody specifically reactive with a sensory receptor family member. For example, a recombinant sensory receptor protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the sensory receptor family.

20 Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring

25 protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

 Methods of production of polyclonal antibodies are known to those of skill in the art. Mice, hamsters, rats, guinea pigs, rabbits, goats, or chickens is immunized with the protein using an adjuvant (*e.g.*, Freund's adjuvant) and a standard immunization protocol with periodic boosts. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of

reactivity to the sensory receptor. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

5 Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511, 1976). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, retroviruses, or other
10 methods well known in the art. Colonies arising from single clones of immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a
15 monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275, 1989.

 Monoclonal antibodies or polyclonal sera are collected and titered against antigen in an immunoassay, for example, a solid phase immunoassay with the antigen
20 immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-sensory receptor proteins, or even other sensory receptor family members or other related proteins from other organisms, using a competitive binding immuno-assay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1
25 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

 Once sensory receptor family member specific antibodies are available, individual sensory receptor proteins can be detected by a variety of immunoassay methods. For a review of immuno-nological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed., 1991). Moreover, the
30 immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

2. Immunological binding assays

Sensory receptor proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patent Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general
5 immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed., 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a sensory receptor family member or an antigenic subsequence thereof). The antibody (e.g., anti-sensory
10 receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent
15 may be a labeled sensory receptor polypeptide or a labeled anti-sensory receptor antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/sensory receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding
20 immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (see, e.g., Kronval *et al.*, *J. Immunol.*, 111:1401, 1973; Akerstrom *et al.*, *J. Immunol.*, 135:2589, 1985). The labeling agent can be modified with a detectable moiety, such as biotin, to which
25 another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the
30 incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a sensory receptor protein in a sample may be either competi-tive or noncompetitive. Noncompetitive immunoassays directly measure the amount of antigen. In one preferred “sandwich” assay, for example, the
5 anti-sensory receptor antibodies are bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the sensory receptor protein present in the test sample. The sensory receptor protein thus immobilized is then bound by a labeling agent, such as a second anti-sensory receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in
10 turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

15 In competitive assays, the amount of sensory receptor protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) sensory receptor protein displaced (competed away) from an anti-sensory receptor antibody by the unknown sensory receptor protein present in a sample. In one competitive assay, a known amount of sensory receptor protein is added to a
20 sample and the sample is then contacted with an antibody that specifically binds to the sensory receptor. The amount of exogenous sensory receptor protein bound to the antibody is inversely proportional to the concentration of sensory receptor protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of sensory receptor protein bound to
25 the antibody may be determined either by measuring the amount of sensory receptor protein present in a sensory receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of sensory receptor protein may be detected by providing a labeled sensory receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay
30 the known sensory receptor protein is immobilized on a solid substrate. A known amount of anti-sensory receptor antibody is added to the sample, and the sample is then contacted with the immobilized sensory receptor. The amount of anti-sensory receptor antibody bound to the known immobilized sensory receptor protein is

inversely proportional to the amount of sensory receptor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, sensory receptor proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the sensory receptor polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percentage cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the sensory receptor family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a sensory receptor family member, to the immunogen protein (*i.e.*, sensory receptor protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to

specifically bind to the polyclonal antibodies generated to a sensory receptor immunogen.

Antibodies raised against sensory receptor conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the sensory receptor family, but not to GPCRs from other families. Polyclonal antibodies that specifically bind to a particular member of the sensory receptor family, can be made by subtracting out cross-reactive antibodies using other sensory receptor family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T2R01 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OLFR1 or mouse OLFR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of sensory receptor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the sensory receptor protein. The anti-sensory receptor polypeptide antibodies specifically bind to the sensory receptor polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-sensory receptor antibodies.

Other assay formats include liposome immunoassays (LIA) using liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34, 1986).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein

compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immuno-assays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, bio-chemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™, fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a sensory receptor protein, or secondary antibodies that recognize anti-sensory receptor.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone,

etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Methods for detecting labels are well known. Thus, for example, where the label is a radioactive label, it may be detected using a scintillation counter or with photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluoro-chrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, with photographic film, or using electronic detectors such as charge coupled devices (CCDs) or photomultipliers. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian sensory, and more particularly, olfactory receptor of the invention, both *in vitro* and *in vivo* are described below, as are methods and compositions for determining whether a test compound is neurotoxic to an olfactory neuron expressing an olfactory transmembrane receptor polypeptide. Any aspect of cell physiology can be monitored to assess the effect of sensant-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical

stimuli into electrical signals. An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and
5 other cognate G-proteins, and modulation of diverse channels by Gi and other G-proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The sensory receptor protein of the assay will typically be selected from a
10 natural poly-peptide or conservatively modified variant thereof. Generally, the amino acid sequence identity will be at least 75%, 85%, 90%, 95%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of a sensory receptor protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand binding domain, subunit association domain, active site, and the like.
15 Either the sensory receptor protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of sensory receptor activity can be tested using sensory receptor polypeptides as described above, either recombinant or naturally occurring. Protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell,
20 expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. *In vitro* binding assays

Sensory perception can also be examined *in vitro* with soluble or solid state reactions, using a full-length sensory receptor-GPCR or a chimeric molecule such as
25 an extracellular domain or transmembrane region, or combination thereof, of a sensory receptor covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of a sensory receptor. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or
30 solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a sensory receptor polypeptide, as well an additional sequence that facilitates the localization of the

sensory receptor to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein.

Ligand binding to a sensory receptor protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Sensory receptors with large (*e.g.*, approximately 600 amino acid residues) extracellular N-terminal segments. These N-terminal segments are thought to form ligand-binding domains, and are therefore useful in biochemical assays to identify sensory receptor agonists and antagonists. Similar assays have been used with other GPCRs, such as the metabo-tropic glutamate receptors (*e.g.*, Han & Hampson, *J. Biol. Chem.* 274:10008, 1999). These assays might involve displacing a radioactively or fluorescently labeled ligand, and measuring changes in intrinsic fluorescence or changes in proteolytic susceptibility, *etc.*

Receptor-G-protein interactions can also be examined. For example, binding of the G-protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor sensant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the sensory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nano-seconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the sensory receptors of the invention, fluorescence-labeled sensants or auto-fluorescent sensants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For

example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley *J. Anal. Toxicol.* 5, 236, 1981 which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$\text{Rotational Relaxation Time} = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (≈ 1 nanosecond) for small molecules (*e.g.*, fluorescein) and large (≈ 100 nanoseconds) for large molecules (*e.g.*, immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Soluble and solid state high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, *etc.*; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; a sensory receptor protein; or a cell or tissue expressing a sensory receptor protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the domain, chimeric molecule, sensory receptor protein, or cell or tissue expressing the sensory receptor is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,

describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

5 Yet another assay for compounds that modulate sensory receptor protein activity involves computer assisted drug design, in which a digital or analog processing system is used to generate a three-dimensional structure of a sensory receptor protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a
10 preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering
15 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a sensory receptor polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of those described herein, or fragments or variants thereof.

20 The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
25 magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the
30 information necessary to form the secondary, tertiary and quaternary structure of the protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent

accessible surfaces, and hydrogen bonding. Secondary energy terms include van der Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the sensory receptor protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of sensory receptor genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used to identify patients having such mutated genes. Identification of the mutated sensory receptor genes involves receiving input of a first nucleic acid or amino acid sequence of a sensory receptor gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once

odorant dependent activation monitored. Control samples (untreated with activators or inhibitors) are assigned a relative sensory receptor activity value of 100. Inhibition of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a sensory receptor protein. One means to determine changes in cellular polarization is by measuring changes in current, and thereby measuring changes in polarization, with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575, 1997). Whole cell currents are conveniently determined using the standard. Other known assays include: assays to measure ion flux using radiolabeled or fluorescent probes such as voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67, 1988; Gonzales & Tsien, *Chem. Biol.*, 4:269, 1997; Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185, 1991; Holevinsky *et al.*, *J. Membrane Biology*, 137:59, 1994). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for G-protein coupled receptors include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists,

antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein coupled receptors, promiscuous G-proteins such as $G\alpha_{15}$ and $G\alpha_{16}$ can be used in the assay of choice (Wilkie *et al.*, *Proc. Natl. Acad. Sci.*, 88:10049, 1991). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature* 312:315, 1984). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (see, *e.g.*, Altenhofen *et al.*, *Proc. Natl. Acad. Sci.*, 88:9868, 1991 and Dhallan *et al.*, *Nature* 347:184, 1990). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors,

serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, sensory receptor protein activity is measured by expressing a sensory receptor gene in a heterologous cell with a promiscuous G-protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995). Optionally the cell line is HEK-293 (which does not naturally express sensory receptor genes) and the promiscuous G-protein is Gal 5 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the sensory receptor signal transduction pathway via administration of a molecule that associates with a sensory receptor protein. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995, may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159, 1994, may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent No. 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent No. 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with ^3H -myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing a sensory receptor protein of interest is contacted with a test compound for a sufficient time to

effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent No. 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase, β -galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, e.g., Mistili & Spector, *Nature Biotech.* 15:961, 1997).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the sensory receptor protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the sensory receptor protein of interest.

6. Transgenic non-human animals expressing sensory receptors

Non-human animals expressing one or more sensory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of translocation domains in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize

odorants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

- 5 Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses.
- 10 When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287, 1997). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of
- 15 one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950, 1997; Scott, *J. Neurophysiol.* 75:2036, 1996; Ezech, *J. Neurophysiol.* 73:2207, 1995. In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and
- 20 medial surface of the turbinates (*see, e.g.*, Youngentob, *J. Neurophysiol.* 73:387, 1995). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1, 1991).

- The sensory receptor sequences of the invention can be for example expressed
- 25 in animal nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *Proc. Natl. Acad. Sci. USA* 96:4040, 1999.

- The endogenous olfactory receptor genes can remain functional and wild-type
- 30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97, 1997). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem (ES) cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53, 1998); Moreadith, *J. Mol. Med.* 75:208, 1997; Tojo, *Cytotechnology* 19:161, 1995; Mudgett, *Methods Mol. Biol.* 48:167, 1995; Longo, *Transgenic Res.* 6:321, 1997; U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries can also be used as reagents to produce "knockout" human cells and their progeny.

F. Modulators

The compounds tested as modulators of a sensory receptor family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a sensory receptor gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by

automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO),
5 Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
10 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

15 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
20 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not
25 limited to, peptide libraries (see, *e.g.*, U.S. Patent No. 5,010,175; Furka, *Int. J. Pept. Prot. Res.* 37:487, 1991; and Houghton *et al.*, *Nature* 354:84, 1991). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, WO 91/19735), encoded peptides (*e.g.*, WO 93/20242), random bio-oligomers (*e.g.*, WO 92/00091),
30 benzodiazepines (*e.g.*, U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.* 90:6909, 1993), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568, 1992), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer.*

Moreover, a method is provided for simulating a fragrance or flavor sensed by a mammal (*e.g.*, human), comprising: for each of a plurality of sensory receptors, or fragments or variants thereof, ascertaining the extent to which the sensory receptor interacts with the fragrance and/or flavor; and combining a plurality of compounds, each having a previously-determined interaction with one or more of the sensory receptors, in amounts that together provide a stimulation profile that mimics the profile for the fragrance and/or flavor. Interaction of a fragrance and/or flavor with a sensory receptor can be determined using any of the binding or reporter assays described herein. The interactions can be aggregated or a profile generated using known signal processing techniques (*e.g.*, a neural network) as described below. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with reporters, chimeric proteins) may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, planar, bead, or fiber) that is solid or porous. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80%, 90%, 95%, 99% or all of the receptors that are substantially stimulated by the fragrance or flavor.

In yet another aspect of the invention, a method is provided in which a plurality of standard compounds are tested against a plurality of sensory receptors, or fragments or variants thereof, to ascertain the extent to which the sensory receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on data storage medium. The method may further comprise providing a desired receptor-stimulation profile for an odor and/or taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the odor and/or taste.

A further aspect of the invention is to provide a method for representing sensory perception of a particular odor and/or taste in a mammal (*e.g.*, human), comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is

greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; and generating from the values a quantitative representation of sensory perception. The sensory receptors may be a receptor disclosed herein, or fragments or variants thereof. The representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, or may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced sensory receptors, or fragments or variants thereof, with a composition and quantitatively measuring the interaction of the composition with the receptors. The maximum number of taste receptors that are needed to mimic the native repertoire (e.g., about 50) may be less than the maximum number of olfactory receptors that are needed (e.g., about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

It is yet another aspect of the invention to provide a method for predicting the sensory perception in a mammal (e.g., human) generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in the mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding known sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is

greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal by comparing the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal to the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal. The sensory receptors used in this method may include a receptor disclosed herein, or fragment or variant thereof. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

Assaying for ligand-receptor binding in a large set of sensory receptors is envisioned to mimic the function of the nose or tongue in sensory perception of chemical sensants. For a set of sensory receptors with a redundancy of ligand-binding domains, the resultant signal is a summation of the interactions of all sensory receptors in the set: none, one, or a few of which have ligand-binding domains that are a perfect fit for the sensant; some of which have ligand-binding domains that are only an imperfect fit for the sensant; and most of which do not significantly bind to the sensant. The individual sensory receptor's binding affinity for sensant varies accordingly. Thus, a suitably large set of ligand-binding domains from sensory receptors will be analogous to any ability of the native repertoire of olfactory or taste receptors to tolerate varying degrees of mismatch between ligand and ligand-binding domain.

The complication of desensitization of sensory receptor signaling will also be avoided by using the invention instead of preparations of nasal or tongue epithelium containing native sensory receptors. For example, the event of binding between ligand and receptor can be separated from more complicated downstream signaling events in the epithelial cells. But the latter events can be reconstituted in the invention by transferring the sensory receptor of interest into appropriate host cells containing an intact and functional signaling pathway.

H. Administration of Novel Sensant Compositions

Sensory modulators can be administered directly to a mammal (*e.g.*, human) for modulation of sensory perception *in vivo*. Administration is by any of the routes normally used for introducing a modulator compound into ultimate contact with the tissue to be treated (*e.g.*, nose or tongue). The olfactory modulators are administered in any suitable manner, optionally with acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Acceptable carriers are determined at least in part by the particular components of the composition to be administered (*e.g.*, stabilizing the sensants), as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed. 1985).

The sensory modulators, alone or in combination with other suitable components, can be made into aerosol formulations (*i.e.*, they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichloro-difluoromethane, propane, nitrogen, and the like that may or may not contribute to sensory perception. Other possible formulation include dry or liquid forms, powders or tablets, solutions of polar (*e.g.*, water) or nonpolar (*e.g.*, alcohol) solvents, emulsions or suspensions, creams, gels, lotions, and syrups.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants; buffers,

bacteriostats, and solutes that render the formulation isotonic, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by orally, topically, intravenously, 5 intraperitoneally, intravesically, or intrathecally. Optionally, the compositions are administered orally or nasally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. The modulators can also be administered as part of a prepared 10 drug, food, or cosmetic. In particular, an unpleasant odor or taste (*e.g.*, sulfur or bitter, respectively) may not be perceived as such and/or its effects reduced by blocking the binding between sensant ligand and sensory receptor by adding a competitor ligand that blocks binding between cognate ligand and receptor, or inhibiting or reducing signal transduction. In contrast, a pleasant odor or taste can be 15 mimicked or enhanced. Primary sensants are preferred because the subset of activated cells is kept small and the effects limited to projection into a specific region of the brain. But novel olfactants or combinations thereof that bind only a few olfactory receptors (*e.g.*, having less than five different ligand-binding domains) would also be useful.

20 The dose administered to a mammal (*e.g.*, human) should be sufficient to effect a beneficial response in the subject over time. The dose will be determined by the efficacy of the particular sensory modulators employed and the condition of the subject, as well as the body weight or surface area of the area to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse 25 side-effects that accompany the administration of a particular compound or vector in a particular subject. In determining the effective amount of the modulator to be administered in a physician may evaluate circulating plasma levels of the sensory modulator, modulator toxicities, and the production of anti-modulator antibodies. In general, the dose equivalent of a modulator is from about 1 ng/kg to 10 mg/kg for the 30 typical mammal. For administration, sensory modulators can be administered at a rate determined by the ED₅₀ of the modulator, and the side-effects of the inhibitor at various concentrations, as applied to the mass and overall health of the mammal. Administration can be accomplished via single or divided doses.

I. Kits

Sensory receptor genes, or fragments or variants thereof are useful tools for identifying cells expressing sensory receptors, for forensics and paternity determinations, and for examining signal transduction in isolated cells. Sensory receptor family member-specific reagents that specifically hybridize to sensory receptor nucleic acids, such as AOFLF1 probes and primers, and sensory receptor specific reagents that specifically bind to a sensory receptor protein, *e.g.*, anti-sensory receptor antibodies are used to examine expression in cells and regulation of signal transduction. For example, one or more family member-specific reagents may be used to detect poly-morphisms that are linked to genetic anosmia or to detect allelic exclusion.

Nucleic acid assays for the presence of DNA and RNA for a sensory receptor family member in a sample include numerous techniques are known to those skilled in the art, such as Southern analysis, Northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybridization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a sensory receptor protein can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant sensory receptor protein) and a negative control.

The present invention also provides for kits for screening for novel modulators of sensory receptor family members. Such kits can be prepared from readily available materials and reagents, as well as any of the aforementioned products. For example, such kits can comprise any one or more of the following materials: sensory receptor nucleic acids or proteins, reaction tubes, and instructions for testing sensory receptor activity. Optionally, the kit contains a biologically active sensory receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

Examples

AOLFR1 sequences:

5 MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVFLGMYLVTVIGNGLIIV AISLD
 TYLHTPMYLFLANLSFADISSISNSVPMKMLVNIQTKSQSISYESCITQMYFSIVFVVIDNLLLGTM
 AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIIALHTLLLIQLLFCNHNTLPHFFCDLAPLL
 KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGWKAFSTCGSHLTVVLLFY
 GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMPINPFYSLRNKDMKGALRKLINRKISSL (SEQ ID
 NO: 1)

10 ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
 CCATCACTGAATTCATTCTCCTGGGATTTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
 GTGCTTTTCTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
 TCAGCTTGGATACGTACCTTCATACCCCATGTATCTCTTCTTCCCAATCTATCCTTTGCT
 GATATTTCTCCTCCATTTCCAACCTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGATC
 15 AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCTCATT
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCATTGTGGCGATCTGCCACCTCTGA
 ATTATAAATTCTCATGCGGCCAGGTTCCGGCATTGTGCTCACAGTCATCTCATGGTTCCTC
 AGTAATATTATTGCTCTGACACACACCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
 CACTCTCCACACTTCTTCTGTGACTTGGCCCTCTGCTCAAACCTGTCCTGTTTCAGATACAT
 20 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTTACACTC
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTTCCACACAGGGAA
 AGTGGAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
 CATTGTAGGCGTGTACTTTTCCCTCTCCACTCACCTGAGGACACTGATAAGATTGGT
 GCTGTCTATTCACTGTGGTGACACCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
 25 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

30 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLLMYVITVVGNLGMIHIIKINPKFHPTPMYFFL
 SHLSFVDFCYSSIVTPKLEENLVMAKSIYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
 NPLLYTVAMSQLCALLVAGSYLWGMFGPLVLLCYALRLNFGSPNVINHFFCEYALISVSGS
 DILIPHLLLSFATFNEMCTLLIILTSYVFIFVTVLKIRSVSGRHKAFTWASHLTAITIFHGTLFL
 YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 3)

35 ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCACCTTTGCCCTTTTAGGTTTCACAG
 ATTACCAAAGCTTCAGATTCTCTCTTCTGTTTCTGCTCATGTATGTTATCAGATG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAAACCCCAAATTCACACTCCTATGT
 ACTTTTCTTAGTCACCTCTCTTTGTTGATTTTGTACTCTTCCACTCCCAAGC
 40 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
 CTTCTGTCTGCACTGCTGTGGTGACAGAGTCTTCTTGTGCTGGCAGTGATGGCCTATGAC
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGGTGCATATCTCTGGGGCATGTTTGGCCCCCTGGTACTCCTTTGTTAT
 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTGTGAGTATACTGC
 45 CCTTCAATGAGATGTGTACACTACTGATCATCCTCACTTCTATGTTTTCATTTTGTGACT
 GTACTAAAAATCCGTTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCTCCACCC
 TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA
 AACTCTCGGCAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
 50 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
 TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

55 MLLTDRNTSGTTFLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL
 LYTVDMSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGNTINHHFCEFSLLSLSCSDTYI

NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTILFLYCV
PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

5 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT
ACCCAGAACTGCAAGTCCCACTCTTCCTGGTTTTCTGGCCATCTACAATGTCAGTGTGCTA
GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT
TTTTCTCAGCCAACCTCTCCTTTGTGGATTCTGTCTATTCTCCATCATTGCTCCCAAGATG
TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTTAGGATGCGTAGTACAATTCT
TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC
10 TTCGTGGCCATTTGCAACCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC
TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC
TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
TACTCTCCCTTTCTTGTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC
TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT
15 CCTCAAGATGCGTTCAGTCAGTGGGCGCGCAAAGCCTTCTCCACCTGTGCCCTCCACCTG
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTTACTGTGTGCCCAACTCCAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

20

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
LLDVMFSSVVPKVVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFICDLFQLTLACTDTHILGL
25 LVTLSNGMMCVAFILILIASYTVILCSLSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

30 ATGGAAAATCAAAACAATGTGACTGAATTCACTTCTTCTGGGTCTCACAGAGAACCTGGAGC
TGTGGAAAATATTTTCTGCTGTGTTCTTGTCTATGTATGTAGCCACAGTGTGAGAAAATCT
ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTTTTTCTTA
CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTGCTTGGCCCCAAGGTGATTGTAGAC
ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCAGCTGTTTGTGGAGC
ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
CATCTGTAAGCCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA
35 GGAGGGGCTTGGGTGGGGGGATTTATGCACGCAATGATACAACTTCTCTTCATGTATCAA
TACCCTTCTGTGGTCTTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTGCGCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCCTGAAGTCT
TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCACCTCACGGTGGTTG
40 TATTGTTCTTTGTCCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTACCCCATGTTG
AAGGCAATGGCTGTGTCAGACTCAATCATCACCCCATGTTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
CTGGGAAATAA (SEQ ID NO: 8)

45 **AOLFR5 sequences:**

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLNLANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSSIIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLAVMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN
ETLLFLVATLNEVVTIMILTSYLLILTILKMGSAGEGRHKAFSTCASHLTAITVFHGTVLSIYCRP
50 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCACTTCTCCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCTGCTGTTCTTCTCATCTATGGAGTCACGTTGTTAGCC
AACCTGGGCATGATTGCACTGATTCAGGTGAGTCTCGGCTCCACACCCCATGTACTTTT
55 TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATTCTACT

TGT TTTGCACTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT
 GTGGCCATCTGTAACCCCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC
 TGGCTTCTTGTCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT
 AGGATCCCCTTCTATAGATCTAATGTGATTAACCACTTTTCTGTGATCTACCTCCTGTCTT
 5 AAGTCTTGCTTGTCTGATATCACTGTGAATGAGACACTGCTGTTCCTGGTGGCCACTTTG
 AATGAGAGTGTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
 GCTATCACTGTCTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCAGTTCAGGCAATA
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCCCTATGCTGAACTC
 10 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
 CAAAATTCACCTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

15 MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 HSLTDFCFSTVVTPKLENLVVEYRTISFSGCIMQFCFACIFGVTETFMLAAMAYDRFVAVCK
 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDLSFCESTFINNFICDHSVIVSASYS
 QRLCFIIAIFNEVSSLIHLTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCV
 NPNTSSLIVTVASVFYTVAIPLNPLIYSLRNKDINNMFEKLVVTKLIYH (SEQ ID NO: 11)
 20 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTGTTCGTCTACACAGTCACTGTA
 GTGGGGAACCTTGGGCATGATAATAATCATCAGACTCAATTCAAACTCCATACAATCATGT
 ACTTTTTCCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTCTCTGGTTGCATCATGCAAT
 25 TTTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTAGAC
 CGTTTTGTGGCAGTTTGTAACCCCTTGCTGTATACCACTATTATGTCTCAGAAAGCTCTGTGC
 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTACATATTTT
 CTTCTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
 AATTGTTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
 30 TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
 TGACAGCCATCACTATCTCCATGGAATATCCTTTTCTTTACTGTGTTTCTAATCCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
 35 CACCAAATTGATTACCCTGA (SEQ ID NO: 12)

AOLFR7 sequences:

40 MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRSKSRDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
 AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFSETKV
 VISYVGCLAQMYYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
 FRVLLMSRLSFCASHIHKHFFCDTQPVLKLSGSDTSSSQMVVMTETLAVIVTPFLCIIFS
 YLRIMVTVLRIPSAAGKWKAFTSCGSHLTAVALFYGSIIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
 PFIYSLRNKDMKRGKLLQDRIYR (SEQ ID NO: 13)
 45 ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA
 CATCTCTCCCACTGCTTCTCCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAAACCTCAGCTGCAG
 AAACCTCTCTTTGCCATCTTCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
 50 CATCCCGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
 TGTCTTTTCATGGATATCTGCTTCAACACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTATGGCAT
 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGCTGGTGGCCATCTG
 CAACCCCTTACACTATGATGTGGTTATGAAACCAACCGCATTGCCTGCTCATGCTATTGGGT
 TCTTGCAGCATCTCCACCTACATTCCCTGTTCGCGTGCTACTTATGTCTCGCTTGTCTTT
 55 CTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCAATTGTGAC

CCCCTTCCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT
 CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACCTCACTGCAGTAGCCCT
 TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGTTAGGG
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCTTTCATCTACAG
 5 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYYFLSH
 10 LSFIDL CYSSVITPKMLVNFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI
 LLFIIGGVNTLATTALVLSYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSIITFMYFKPPSS
 TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTGRGRQS (SEQ ID NO: 15)

ATGGCTACTTCAAACCATTCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
 CAGAACCTCAACTGCCACTCTTCCTCCTGTTCTTGGAATATATGTGGTCACAGTGGTGGG
 GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGTATTATT
 TTCTCAGTCATTTGTCTTTTCATTGATCTCTGCTACTCCTCTGTCATTACCCCTAAGATGCTG
 GTGAACTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
 20 CTTCTTATTTTTGTAAATTGCAGAAAGGTACCTTGTGTCATGTCCACAGGGTCTGTTCCATAAT
 GTTGCTATCTGTGCGCCACTGCTTTACAATATTTGTGTCATGTCCACAGGGTCTGTTCCATAAT
 GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
 GTGTTGTCATTCTGTAGGTCTCATAACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT
 GACTCTGTCTTGTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTGGAGGAGTT
 25 AATACCTTAGCAACTACACTGGCGGTCTTATCTCTTATGCTTTCATTTTCTCTAGTATCCT
 TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCATCTCTTG
 GCTGTGGGCATCTTTTTTGGGTCTATAACATTCATGTATTTCAAGCCCCCTTCCAGCACTAC
 TATGAAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
 CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
 30 AGGCAGTCATCCTGA (SEQ ID NO: 16)

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQFFFLFLVIYIVTMVGNLGLITLFLGLNSHLHTPMYYFLFN
 LSFIDL CYSSVFTPKMLMNFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
 35 LYKVTMSHVQCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYCDILPLLQLSCTSTYV
 NEVVVLIVGTNITVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
 SSGSMEQKGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAAACAGATCGTC
 CAGAGTTCTGGCAACCCTTCTTTTTCTGTTCTTAGTGATCTACATTGTCACCATGGTAGGC
 AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAATGCTAAT
 GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
 TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
 45 GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG
 ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTCC
 AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
 TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTATTGTCAGTACTAGCATTCTTC
 50 ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTGC
 TCTGTCTCTGTTTTTTGGGTGAGCGGCATTCATGTATATTAAATATTCTTCTGGATCTATGG
 AGCAGGAAAGGTTTTTTCTGTTTTCTACATAATGTGGTGCCCATGCTCAATCCCCCTCATC
 TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAG
 AGGAGAAATATATTCTAA (SEQ ID NO: 18)

55

AOLFR10 sequences:

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLILFGLNSHLHTPMYYFLFNL
 SFIDLCYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMA YDRYVAICNPLLY
 KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLRTFCSANINHYLCDILPLLQLSCTSTYVN
 5 EVVVLI VVGINIMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
 SGSMEQKGKVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
 CAGAGTTCCGGCAACCCCTCTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
 10 AACCTTGGCTTGATCATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATT
 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTCACTCCCAAATGCTAAT
 GAACCTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT
 TTCTCTTTTTTGTCTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
 GCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCAC
 15 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA
 CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
 GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTGTCTCATTGTTGTGGGTATTAAT
 ATCATGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTCACTAGCATTCTTCA
 TATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGCTATGCT
 20 CTGTCTCTGTTTTTGGGTGAGCGGCATTATGTATATTAATATTCTTCTGGATCTATGGA
 GCAGGGAAAAGTTTCTTCTGTTTTCTACATAATGTGGTGCCCATGCTCAATCCTCTCATCT
 ACAGTTTGAGGAACAAGGATGTCAAAGTGCAGTGAAGGCTCTGATTAAAATTCAGA
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNL
 FIDLCYSCVFTPKMLNDFVSEHSISYVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPLLY
 MVTMSPRVCFLLMFGSYVVGFAAGAMAHTGSMRLRTFCDNSNVIDHYLCDVLPPLLQLSCTSTHV
 30 SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIAVALFFGSGTFTYLTTS
 FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTTGGGATTATCAGAACAGC
 CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
 35 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCCATGTACTTTTT
 CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGTGTGTTACCCCCAAATGCTGA
 ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC
 TGTTCCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTCTGCTGATGT
 40 TTGGTTCCTATGTGGTAGGGTTTGTGGGGCCATGGCCCACTGGAAGCATGCTGCGACT
 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGACG
 TCTCCTGCACCAGCACCCATGTCAAGTGAGCTGGTATTTTTTCACTGTTGTTGGAGTAATCACC
 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCATATGGGGTCCCACATAATTGCTGTT
 GCTCTGTTTTTTGGGTGAGGGACATTACCTACTTAACAACATCTTTTCTGGCTCTATGAA
 45 CCATGGCAGATTGCTCAGTCTTTTACACCAATGTGGTTCCCATGCTTAACCCTTCGATCT
 ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT
 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDCNVLNFFADKKNKRNFQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL
 50 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLIILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV
 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYITIMSHRCCVLLLVLS
 FCIPHFSLLHILLTNQLIFCASNVIIHFFCDDQPVLLKSCSSHVKEITVMTEGLAVIMTPFSCIII
 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
 55 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTCTTTGCTGATAAGA
 AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAGACCCTCTGA
 ATTCATCCTCCTTGGACTCTCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
 5 TCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTGACATTTGCT
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
 10 CCATTATGAGTCACAGATGCTGTGCTCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
 TCATTCTTCTGCGATGATCAACCAGTGCTAAAATTGCTGTTCTCCTCCCATTTTGTCAAAAG
 AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT
 CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCTTTCAGCTGCTGGAAAGCGTAAA
 15 GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCTGTTTTATGGAAGCATTAGCTA
 TGTCTATTTTCAGCCCTGTCCAACTATACTGTCAAGGATCAAATAGCAACAATTATCTAC
 ACCGTA CTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
 AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTGAGTAA (SEQ ID NO: 24)

20 **AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTIIVLSHLDPHLHNP MYFFFSNL
 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
 HYTVVMHPCLYVLMASWVIGFANSLQLTVLILLTLGRNKLHFLCEVPPLKLACVDTT
 MNESELFVSVIILLVPVALIIFSYSQIVRAVVRKISATGQRKVFGTCGSHLTVVSLFYGTAIYAY
 25 LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNDVKGALKKVLWKNYDSR (SEQ ID NO:
 25)

ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
 CTCAGCTGGAGCTAGTCCTCTTTGTGGTTTCTTTGATCTTCTATATCTTCACTTTGCTGGGG
 30 AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTTT
 CTTCTCCAACCTAAGCTTTTTGGATCTGTGTACACAACCGGCATTGTTCCACAGCTCCTGG
 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTGTGTAGTTTCAGCTGTACAT
 CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
 GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA
 35 TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
 CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCTCCATTGCT
 CAAGCTTGCTGTGTTGACACTACTATGAATGAATCTGAACCTCTTCTTTGTGAGTGTCTATTA
 TTCTTCTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG
 AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCACCTCACA
 40 GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTTACCTCCAGCCCGGCAACAACTACTC
 TCAGGATCAGGGCAAGKTCATCTCTCTTCTACACCATCATTACACCCATGATCAACCCC
 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
 AACTACGACTCCAGATGA (SEQ ID NO: 26)

45 **AOLFR14 sequences:**

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLPRATIPYTACALQMF
 VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLLCLALLGASGLGAVSAFVHTTLTF
 RLSFCRSRKINSFFCDIPPLLAISCDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
 50 GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALD TDKMASVFYTLVPSLNPLIYSLRKE
 VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
 GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCTCCTGGGC
 55 ATCACAATCGCTGGGACCTGCGTGTGGCCCTCTTCTGACCTGCCTGCCTGTCTACCTGG
 TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA

CACCTATGTACTTCTTCTGCGCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
CCCTCCAGATGTTTGTCTTTGCAAGTCTGGCTGATACTGAGTGTGCTTGTGCTGGCAGCCAT
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTCGAG
5 CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTC
ACACAACCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGCTGGCCATCTCGTGCACTGACACCAGTCTCAATGAACCTCTTCTCT
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTAGCTATCACGGTGTCTTATGGCTT
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTCGGCGAGCAGCTCCAC
10 CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG
TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGTCCCAGTGA (SEQ ID NO: 28)

15 **AOLFR15 sequences:**

MRENNQSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNPMPYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHLLTASLSFCGNQEVANFYCDITPLKLSGSDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLEYGTVMGTYFR
20 PLTNYSLKDAVITVMTAVTPMLNPFYISLRNRMKAALRKLFNKRIS (SEQ ID NO: 29)

ATGAGGGAAAATAACCAGTCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTCTTCTACATCCTCTTCTGTTCAATTAACCCATCACATTGATTGGA
AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTGCGCTTCAACCCCATGTATTTCT
25 CCTTGCCAACCTCTCCTTGGTTGACATCTTCTCTCATCGGTAACCATCCCTAAGATGCTGG
CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC
30 TAGTCTGTCTTCTGTGGCAACCAGGAAGTGCCAACTTCTACTGTGACATTACCCCTTG
CTGAAGTTATCCTGTTCTGACATCCACTTTTATGTGAAGATGATGTACCTAGGGGTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTTGTCTCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCACCTCAGGT
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC
35 TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTTCAT
CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

40 **AOLFR16 sequences:**

MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAGNLMIVLIQANAWLHMPMYFFLSH
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLQCYLFIALVHVEIYILAVMAFDYMAICNPLL
YGSRMKSVCFLITVPYVYGALTGLMETMWTYNLAFCGPNEINHFCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFIICISYLYIFAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
PPSKESVEQGKMVAVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

45 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG
GAATTACAAATTCTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTC
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG
50 AGATTTTCTTTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGCACTGTACCTT
TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCTC
ATCACGGTGCCTTATGTGTATGGAGCGTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAGTTAATCACTTCTACTGTGCGGACCCACCACTGAT
55 TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
AACCTTTCTTTTCTCTCTCATCATATGATTTCTACCTTTACATTTTCCCTGCTATTTTA

AAGATTTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCTCAAAGGAATCT
GTTGAACAGGGTAAATGGTAGCTGTATTTATACCACAGTAATCCCTATGCTGAACCTTA
5 TAATTTATAGCCTTAGAAATAAAATGTAAAGAAGCATTAAATCAAAGAGCTGTCAATGA
AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVTEFILLGLTSRREWQVLFHIFLVVYIITMVGNIGMMVLIVSPQLNNPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFIALVHVEIFILAAMAFDRYMAIGNPLL
10 YGSKMSRVVCIRLITFPYIYGFLTSLAATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKE
YTMILAGINFYSLTVIISYLFILAILRMRSAGEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
15 GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCTCA
GTCACTTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTAGATAAAAAAACAATTACTTATGCTGGTTGTTTAGTACAGTGTCTTCTTCTCAT
TGCTCTTGCCATGTGGAAATTTTATTCTTGTGCGATGGCCTTTGATAGATACATGGCAA
20 TTGGGAATCCTCTGCTTTATGGCAGTAAATGTCAAGGGTGTCTGTATTGACTGATTAC
TTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACTTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATGTCCGCAAT
25 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

30

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVYVLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFLVLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
35 EHAMFISAGFNLSSSLTIVLVSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTFLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
40 CGGAAGTCCAGTCTCTGCTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
45 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTATATCTGCTGGCTTCAAC
CTCTCCAGTCCCTCACCATCGTCTTGGTGTCTATGCCTTCATTCTGCTGCCATCCTCCG
GATCAAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC
50 TGTCACCCTGTTTTATGGGACTCTCTTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

55

AOLFR19 sequences:

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLIILAIYSDPRLHTPMYFFLSNL
 SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
 YDVVMKPWHCILLMLLGSCSISHLHSLFRVLLMSRLSFCASHIHKHFFCDTQPVCLKLSCSDTSSSQ
 5 MVVMTETLAIVITPFLCTIFSYLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVYFR
 PLSMYSVMKGRVATVMYTVVTPMLNPFYISLRNKDMKRGLKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
 ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTCCTCATCATGTACCTACTCACTGCGGTG
 10 GGGAAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
 TTTTTCTCAGCAACTTGTCTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATG
 CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT
 ACTTCTTCATGGCATTGTTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 15 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTCTGTGCCTCTCACATCATTAAGCACTTTTCTGTGACACCCAGCCTG
 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
 TGCTCAGAATCCCCTCTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCT
 20 CACTGTAGTGGTCTGTCTATGGGAGTGTCTATGTCTATTTTAGGCCTCTGTCCATGT
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
 ACCCTTTCTATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTHPELKTLLFVVFFAIYLLITVVGNISLVALIFTHCRLHTPMYIFLGN
 LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRVFCGLNHINHFYCDTLPYRLSCVDPF
 30 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
 NLLEEGGNDIPAILFTIVVPLLNPFIYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCCTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCCGCTTCACACACCAATGTACATC
 35 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGCTGTGCCTGTGCTATTACCCCAAAATGTT
 AGAGAACTTCTTTCTGAGGGCAAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
 TTTCTTTGCACTGTGGAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCCTTCATAGCTGGAAATCTGCATTCCATGATTTCATGTAGGGCTTGTA
 40 TTTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTGACCTTTTCATCAATGAAGTGGTCTATTTCATCTTCTCAGGTT
 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTTGTGCATCCCACTTTT
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA
 45 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTTCTGCTGAA
 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDVFLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL
 50 TFIDIIYSSSISPRLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMAYDRYVAICKPLHYLV
 IMRQWVCVLLLVSWSVGGFLQSVFQLSIHYGLPFCGPNVIDHFFCDMYPLKLACTDTHVIGLL
 VVANGGLSCTIAFLLLLISYGVLHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

55

TCACCCCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCACCCCTG
 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
 TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCCTATCTGCTCATCATCAAGACCATT
 TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
 5 CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
 TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTGCTAGGA
 GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

10 **AOLFR25 sequences:**

METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIITVTSDSQLHTPMYFLLRN
 LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL
 RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLR LACTDT
 SLLEFLKISNSGLLDVWVFFLLMSYLFILVMLRSHPGEARRAASTCTTHIIVSMIFVPSIYLY
 15 ARPFTPFMDKLV SIGHTVMTPMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

ATGGAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCTGTTGGGCTCTCGCAGACTC
 GGGAGCTCCAGCGTTTCTGTTTCTAATGTTCTGTTTGTCTACATCACCCTGTTATGGGA
 AACATCCTTATCATCATCAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT
 20 GCTCCGAAACCTGGCTGTCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAAATGCTAG
 TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
 CTTCACCTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGATGGCCTTTGACCGCCTCA
 TTGCCATCTCCCGGCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
 GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
 25 CCACTGCCCTTCTGTGGCCCCAACATTTTGGATAACTTCTACTGTGATGTTCCCCAAGTACT
 GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
 CTGGATGTCGTCTGGTCTTCTCCTCCTCTGATGTCTACTTATTCATCCTGGTGATGCTGAG
 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT
 GGTTCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
 30 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCCATGCTCAACCCCATGATCTA
 TACCTGAGGAACCAAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
 TTGA (SEQ ID NO: 48)

AOLFR26 sequences:

35 MAAKNSSVTEFILEGLTHQPGLRIPLFFFLGFFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
 LIDFCFSTTITPKMLMSFVSRKNIISFTGCMTQLFFFCFFVSESFILSAMAYDRYVAICNPLLYT
 VTMSCQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPILLESCNSSYMN
 ELVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP
 40 LSILPLEQGVSSLFYTIIVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
 GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
 CCTGGGCTTGATAACCCTGATTGGGCTGAACTCTCACCTGCACACTCCCATGTACTTCTTCC
 TTTTAACTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG
 45 AGTTTTGTCTCAAGGAAGAACATCATTTCTTTCACAGGGTGTATGACTCAGCTCTTCTTCTT
 CTGCTTCTTTGTCTCTCTGAGTCCCTCATCCTGTCAGCGATGGCGTATGACCGCTACGTGG
 CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG
 TTGGGTGCCTATGGGATGGGGTTTGTGGGGCCATGGCCACACAGGAAGCATAATGAAC
 CTGACCTTCTGTGCTGACAACCTTGTCAATCATTTTCTGTTGATCATCTTCTCTCTTGA
 50 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
 GTTGAATGCCCATTTGCTACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA
 CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTCCACATAATTGTA
 GTTTCTCTTTTCTTTGGTTCTGGTGTCTTTCATGTATCTCAAACCCCTTCCATCCTGCCCTC
 GAGCAAGGGAAAGTGTCTCCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA
 55 TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
 TCTTTTCTTAA (SEQ ID NO: 50)

AOLFR27 sequences:

- MPSQNYSHSEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIEHRLHTPMYFLCTL
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
5 YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIHHFFCHVLSLLKLACENKT
SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHTYSFASFIY
LKPKGLHSMYSDALMATTYTVFTPFLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
51)
- 10 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
CCAGCACCTCCTGCCCATCTTGTTCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
CTTCTTGTCACCCCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC
TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACAGATGTTCT
15 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCCTGATGATGGGCTATGATCGCTA
TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGACTGTGCCCAT
CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTCTGTGATGTGCTTTCCCTCT
TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTATCATGGGTGTGATGTGCTGTGTGT
20 CAGAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCTTCATTGTGGCTGCCA
TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCCACCT
CACTGTGGTGGTCACGCACTATAGTTTGCCTCCTTTATCTACCTCAAGCCCAAGGGCCTCC
ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCACCCCCTTCTTAGC
CCAATCATTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACCTTTTACA
25 GAAAATTCTGTCCTCCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

- MPNFTDVTFTLLGLTCRQELQVLFFVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSE
ADVCFSNVTPKMLENLLSETKTISYVGCLVQCYFFIAVVHVVEVYILAVMAFDRYMAGCXPLL
30 YGSKMSRTVCVRLISVXYXYGFSVSLICTLWTYGLYFCGNFEINHFCADPPLIQIACGRVHIKE
ITMIVIAGINFTYSLSVLISYTLIVVAVLRMRADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
RPTEESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)
- 35 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCGTCAGGAGC
TACAGGTTCTCTTTTTGTGGTGTTCCTAGCGTTTACATGATCACTCTGTTGGGAAATATT
GGTATGATCATTTTGTATTAGCATCAGTCCTCAGCTTACAGAGTCCCATGTACTTTTCTGAG
TCATCTGTCTTTTGGCGACGTGTGCTTCTCCTCCAACGTTACCCCCAAAATGCTGGAAAAC
TATTATCAGAGACAAAAACCATTTCTATGTGGGATGCTTGGTGACGTGCTACTTTTTCAT
TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
40 GGCTGCAANCCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCCGGCTCATCT
CTGTGNNNTATGNNNTATGGATTCTCTGTGACGCTAATATGCACACTATGGACTTATGGCTT
ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
TTGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT
CACATATCCCTCTCGGTGGTCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA
45 TGCGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT
TTCTATGTTTTATGGGACCCCCATCTTCATGTATCTCAGGAGACCACTGAGGAATCCGTA
GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA
TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAGACAT
ATGTGAGGCAGTAA (SEQ ID NO: 54)

50

AOLFR29 sequences:

- MMSFAPNASHSPVFLLLGFSRANISYTLFLFLAIYLTTLGNVTLVLLISWDSRLHSPMYYLLR
GLSVIDMGLSTVTLPLQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
PLHYALVMNHQRCACLLALSWWVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR
55 ASCSDIHSNELAIFFEFGFLMLGPCALIVLSYVRIGAAILRLPSAAGRRAVSTCGSHLTMVGFL

TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT
 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA
 TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCTGGAGTCTGCATCATCT
 5 TAGTGGGCATGTCCTACCTGGGTGGATGTGTGAATGCTTGGACATTCATTGGCTGCTTATT
 AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTCTGTGACTATTCACCACTTT
 TGAAGCTTGCTTGTTCCTCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT
 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
 10 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
 GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
 AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
 AAAATATTTTCTTGA (SEQ ID NO: 60)

15 **AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSHILIRISSQLHHPMYFFLSHLAFADM
 AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
 MSTQVSVQLLL VVYIAGFLIAVSYTTSFYFLFCGPNQVNHFFCDFAPLLELSCDISVSTVVLSF
 20 SSGSIHVTVCVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
 DQNKVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
 NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
 25 ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
 GGCTTTTGTGACATGGCCTATTCATCTTCTGTACACCCAACATGCTTGTAACCTTCCTGG
 TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
 TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGCCAGCTACTCTTAGTAG
 30 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCTTCTATTTTTTACTCTTCT
 GTGGACCAAAATCAAGTCAATCATTTTTTCTGTGATTTTCGCTCCCTTACTTGAACCTCTCCTGT
 TCTGATATCAAGTGTCTCCACAGTTGTTCTCTCATTTTCTTCTGGATCCATCATTGTGGTCA
 TGTGTGTGTCATAGCCGCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
 CTGAGGGGGCACCACAAGGCCTTCTCCACCTGCACCTCCACCTCACTGTGGTTACCGTGT
 35 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
 ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

40 **AOLFR34 sequences:**

MLEGVEHLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVIYLLTVSGNG
 LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT
 ECFlyTLMA YDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSLFQTSFVFRLPFCGPNRV
 45 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYVAAILRIPSADGRRNAFST
 CAAHLTVVIVYYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIHYTLCNKEMKAALQRLGG
 HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
 AACTGCAAAGTGGAACAGACTTCTGTGTCTCACTTCATTTGGTGGGCCTGCACCACCC
 50 ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCTTGTCTATCTCCTCACTGTTTCTG
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
 GTTCTGTGTCACTCTCCTTCTTGGACATGACCATTTCTTGTGCTATTGTCCCAAGATGC
 TGGCTGGCTTTCTTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAACATTT
 TCTTTCCATTTCTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT
 55 CTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
 TGGCTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTCCAAACAAGTTTTGTATT

CCGGCTGCCCTTCTGTGGCCCCAATCGGGTCGACTACATCTTCTGTGACATTCCCTGCCATGC
 TCGCTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT
 CCTGGCCCTCACCTGCTTCATGCTCATCTCACTTCTATGGCTATATTGTAGCTGCCATCC
 TGCGAATTCCGTCAGCAGATGGGCGCCGAATGCCTTCTCCACTTGTGCTGCCACCTCAC
 5 TGTGTGCTATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTCACAGGAGC
 CCCTGGATGGGGTGGTAGCTGTCTTTTACACTGTCATCACTCCCTTGTCTAACTCCATCATC
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
 GTGCAGCCTCACTGA (SEQ ID NO: 64)

10 **AOLFR35 sequences:**

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLTGNTAIMAVSVLDIHLHTPVYFFLG
 NLSTLDICYTPTFVPLMLVHLLSSRKTISFAVCAIQMCLSLSTGSTECLLLAITYDRYLAICQPL
 RYHVLMSHRLCVLLMGAAWVLCCLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT
 SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIIFMY
 15 LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO:
 65)

ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC
 CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCTCCTGGG
 20 GAACACAGCCATCATGGCGGTGAGCGTGTAGATATCCACCTGCACACGCCCCGTGACTTC
 TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCCACCTTTGTGCCTCTGATGCT
 GGTCCACCTCCTGTCTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
 TGAGCCTGTCCACGGGCTCCACGGAGTGCCTGCTACTGGCCATCACGGCCTATGACCGCTA
 CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGCTG
 25 CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
 TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT
 GCTGAAGCTGGCATGCGGCAACACGTCCGTCAGCGAAGACTTCCTGCTGGCGGGCTCCAT
 CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTCTACTGCTCATCTGGCCACCA
 TCCTGAGGGTGGCCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT
 30 GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCTGCTACTTGAAGCCCAAGAGTAAG
 GAAGCCACATCTCTGATGAGGTCTTACAGTCTCTATGCCATGGTACGACCATGCTGA
 ACCCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
 GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

35 **AOLFR36 sequences:**

MYLVTVLRLNLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
 CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS
 WIVLQFTFFKNVEISNFVCEPSQLLKLASVDSINSIFYDNTMFGFLPISGILLSYKIVPSILRIS
 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFYIS
 40 LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTGACGTCTGACTCCC
 ACCCCACACACCCATGTACTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
 TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTGCATAGCAAAGTCATCTCTTATG
 45 GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCTT
 GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCGCCCTCTGCACTACCCAGTCATC
 GTGAATCCTCACCTCTGTGTCTTCTTCGTTTTGGTGTCCTTTTTCTTAGCCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCTAATT
 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCTCTTATGACAGCGTCATCAATAGCATA
 50 TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTCAGGGATCCTTTTGTCTTAC
 TATAAAATTGTCCCCTCCATTCTAAGGATTTTCATCATCAGATGGGAAGTACAAAGCCTTCT
 CAGCCTGTGGCTGTACCTGGCAGTTGTTTGTCTATTTTATGGAACAGGCATTGGCGTGA
 CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
 GTGGTCACCCCATGCTGAACCCTTTCATCTACAGCCTGAGAAACAGGACATTCAAAGTG
 55 CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG

TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCCTTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

5 MEKANETSPVMGFVLLRLSAHPELEKTFVLLIMYL VILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSFLTPQETISFSACAVQMALSFAMAGTECLLLSMMAFDRYVAICNP
LRYSVIMSKAA YMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPVLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLLFFMYG
10 KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIIYSLRNKDVKA A VRRLLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
GGGCAATGGGGTCCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCCATGTAC
15 TTCTTCCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT
CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGTGATC
GCTATGTGGCCATCTGCAACCCCTTAGGTA CCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
20 GCAATTGAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTACCTGTGAGATTCTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
TGTGATCTTCTAGGAGTCCCGGTTCTGTTTCTCTTCTCCTATGTCTTCATCATCACCA
CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
25 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG
GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

30 MYLVTVLRNLLILA VSSDSLHTPMCFFLSNLCWADIGFTSAMVPKMIVDMQSHSRVISYAGC
LTQMSFFVLFIACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFTYLD SIMFGFLPISGILLSYANNVPSILRISS
SDRKS KAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPFYISLR
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

35 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTCTTTGTCTTTTGCATGTATAGAAGACATGCTCCTG
40 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCAACCCCTGCACTACCCAGTCATCA
TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCCTCAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAAATGTGGAAATCTCCAATT
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCTGTTCTGACAGTGTCAATAGCATA
TTCATATATTTAGATAGTATTATGTTTGTCTTCTTCCATTTCAAGGATCCTTTTGTCTTAC
45 GCTAACAAATGTCCCCTCCATTCTAAGAATTCATCATCAGATAGGAAGTCTAAAGCCTTCT
CCACCTGTGGCTCTCACCTGGCAGTTGTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGTCAACACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
GTGGTCAACCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
50 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLLSGLTEQAELQLPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVISSECYMLAAMACDRYVAICSPL
55 LYRVIMSPRVCSLLVA AVFSVGFTDAVIHGGCILRLSFCGSNIKH YFCDIVPLIKLSCSSSTYIDEL

LIFVIGGFNMVATSLTHSYAFILTSILRIHSKKGRCFAFSTCSSHLTAVLMFYGSLMSMYLKPAS
SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

5 ATGGGTGTAAAAAACCATTCACAGTGACTGAGTTTCTTCTTTCAGGATTAACGAACAAG
CAGAGCTTCAGCTGCCCCCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCCATGTACTAT
TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCAATTACCCCTAAAAATGCT
ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTAGCTGTTTT
TTTTCTGTGTTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
10 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT
CAGGTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCCTCTTA
TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTGTCAATTGGTGGATTT
AACATGGTGGCCACAAGCCTAACATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT
15 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCACCTGACA
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC
ACTACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

20

AOLFR40 sequences:

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS
25 ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL
RPGSRDALHGVVAVFYTTLTPLFNPVVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

30 ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCTA
CCAACCTGTCTTCATTGACATGTGGTCTCCACTGTACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCTATGATCGCTACCT
35 GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
GCCACCGGCACCTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT
40 GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTTGTGGCCGTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

45

AOLFR41 sequences:

MNPENWTQVTSFVLLGFPSSHLIQFLVFLGLMVYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLTVVVVPKMLVVILTGDHTISFVSCIHSYLYFFLGTTDFLLAVMSLDRLAICRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLRLSCGDTH
50 LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTA AERRKAFSTCASHLTVVVIYGSSIFLY
IRMSEAQSKLLNK GASVLSCIITPLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

55 ATGAACCCTGAAAACTGGACTCAGGTAACAAGCTTTGTCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCTGCTGTTCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC

TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
 TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTGAGCTGCATCATCCAGTCCTACC
 TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCTTGGCCGTCATGTCTCTGGATCGTTAC
 CTGGCAATCTGCCGACCACTCCGCTATGAGACCTGATGAATGGCCATGTCTGTTCCCAAC
 5 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCCTTTGCCCACTGTCTCATGGCC
 AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCTGTGACAGTTGGCCCTTGCT
 CAGGCTTTCTTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTCATGCTCTCTACGTTG
 GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCCTGCATTCTTGCCACTGTTCT
 CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTCCTACTTGCGCCTCGCATCTTACA
 10 GTGGTGGTCATCATCTATGGCAGTTCCATCTTTCTCTACATTTCGTATGTCAGAGGCTCAGTC
 CAAACTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA
 TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
 CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO: 78)

15

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFHFIGGIKIFLLTVMAYDRYIAISQPL
 HYTLIMNQTVCALLMAASWVGGFHISIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV
 20 LELLMVSNNGLVTLMLCFLVLLGSYTALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIVYVY
 TRPFR:TFPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
 (SEQ ID NO: 79)

ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
 25 GGGAGCTTCGGTTTGTCTTCTTCACTGTTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT
 CTTGGGCAATCTTTCTTCTTCTGGACTTTTGTCTACTCTTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCCTACCATTTCTTTGGTGGATGCCTGACTCAACTCTTCTTC
 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCTGTCATGGCGTATGACCGCTACA
 30 TTGCCATTTCCCAGCCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGGCTTCACTCCACTCCATAGTACAGATTGCATTGACTATCC
 AGCTGCCATTCTGTGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAAATGGCCTG
 GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
 35 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTTGTGCCTTGCATCTACGTCTATAACAAGGCCTTTTCGGACATTCCCCA
 TGGACAAGGCCGCTCTGTGTGCTATACACAATTGTCAACCCCATGCTGAATCTGCCATCTA
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

40

AOLFR43 sequences:

MQKPQLLVPIATSNLNLVHAAFYLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHALSAVESAVLLA
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSCYQHTVTHSFCLHQ
 45 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCAV
 LVFYVPLIGLSVHRLGGPTSLHVMANTYLLLPPVVNPLVYGAKTKEICSRVLCMFSSQGGK
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 50 CAGCATACTTCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACTTTTGGCTGGCT
 TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGCTCTCATCAT
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
 GACCTAGTCTCTCTCTATCACCATGCCCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA
 GGAGATCGAGTTCAACATTTGCCTGGCCCAGATGTTCTTATCCATGCTCTGTGAGCCGTG
 55 GAGTCAGCTGTCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC
 GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG

GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCCTACTGCCAAACAC
ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCCTGTACTGACAC
CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCCTCTCGGAGGGCA
5 GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGTT
ATGGCTAATACCTACTTGCTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
NO: 82)

10

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGNCIVVFIVRTERS LHAPMYLFLC
MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHLSAIESTILLAMAFDRYVAICHPL
RHA AVLNNVTVAQIGIVAVVRGSLFFFLPLLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
15 NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLS
VVHRFGNSLHPIVRVVMGDIYLLPPVINPIHYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
20 AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTCCCATGTATGTAGTGGCAATGTTTGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
25 CCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCCTCTCGACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTTATTTTCTGATAATACGAACGGTTCTGC
30 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTGT
GGTACTCGCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
CTTCATCCCATTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA
TCCCATCATCTATGGTGCCAAAACCAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

35

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA
MLATIDLVLSSSTLPKMLAIFWFRDQENFFACLVMFFLHFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTVLSLITKIGMAAVARAVTLMTPFLRLRFHYCRGPVIAHCYCEHMAVVRLACGDT
40 SFNNYGIAMFVSVLDDLFLVLSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIHYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

TGGAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
45 CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
TCCTGGTTTGGAAACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCCTTCTCTTCAATTATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC
50 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCTGACTGGGTCCCTC
ATCACAAGATTGGCATGGCTGCTGTGGCCCGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA
55 CATGGCTGTGGTAAGGCTGGCGTGTGGGCACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTGTAGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT

TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCGCTACAAAGCATTGGGACATGTGTG
 TCTACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
 TGTAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCGTGAGTATGTGCT
 5 CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
 AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
 ATCTTTGACAATTCTTAGTATGATAAGGAAAATGAGGTTTCATTCTCAGATCTACGA
 GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
 TTGTCATAGACTCATCACATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
 10 GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
 NO: 86)

AOLFR46 sequences:

MNIKHCGWHMIHTWLNIREDDSDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
 15 SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQLAS
 LHQPLYLLSLSLLDIVLCLTVIPKVLAIWFDFLRSISFPACFLQMFIMNSFLTMESECTFMVMA
 YDRYVAICHPLRYPSTTDQFVARAVVFVIARNAFVSLPVPMLSARLRYCAGNIKNKICSNLSVS
 KLSDDITFNQLYQFVAGWTLLGSDLILIVISFILKVVLRJKAEGAVAKALSTCGSHFILILFFS
 TVLLVLVITNLARKRIPDPVILLNHLHLLPALNPVYGVRTKEIKQGIQNLKRL (SEQ ID NO:
 20 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
 GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT
 CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
 25 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCC
 CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
 CTGCCCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
 CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG
 ACATCGTGCTCTGCCTCACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
 30 TCGATCAGCTTCCCAGCCTGCTTCCCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
 GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
 TACCCGCTCATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
 ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
 ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAAACTCTTGTGTATGACATCA
 35 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
 ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
 GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC
 TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT
 40 GCTCAACATCCTGCACCACCTCATTCCCCAGCTCTGAACCCCATGTTTATGGTGTGAGA
 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA
 45 MLAAIDLVLSSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
 PLHYTKVLTGSLITKIGMAAVARAVTLMTPLPFLLRFCFHYCRGPVIAHCYCEHMAVVRACGD
 TSFNNIYGIAVAMFIVLDLLVILSYIFILQAVLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
 SVMHRVARHAAPHVHILLANFYLLFPPMVNPIIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
 89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTGGTGGGGATTCCAG
 GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
 CTTGGAACCTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
 ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCTCCTCAGCACTGCCAAA
 50 ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCAGGA
 TGTCTTCTCCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
 55 CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA

CCAAGATTGGCATGGCTGCTGTGGCCCCGGGCTGTGACACTAATGACTCCACTCCCCCTTCCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
5 GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAAGTGTGGTCATCTCTTCAGTCATGCACCGTGTA
GCCCCGCATGCTGCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCCATATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGA
GTATCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

10

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTHIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH
PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI
15 RVNVVYGLVHSAIGLDSLLISFSYLLILKTVLGLTREAAKAFGTCVSHVCAVFIFYVPFIGLSM
VHRFSKRDRSPLPVILANIYLLVPPVLNPVYGVKTKAIRQLRLRFHVATHASEP (SEQ ID NO:
91)

ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
20 CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
25 GACCGCTATGTGGCCATCTGTACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATGGTGTGGCTGCTGTGGTGGGGGGGCTGCACTGATGGCACCCCTTCCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
30 AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTTGGCACTTGCCTCTCTCA
TGTGTGTGCTGTGTTTCATATTCTATGTACCTTTTATTGGATTGTCCATGGTGCATCGCTTGA
GCAAGCGGCGTGACTCTCCGCTGCCCCGTCATCTTGCCCAATATCTATCTGCTGGTTCCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGCATCCTTCGA
CTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

35

AOLFR49 sequences:

MLTFHNVCSVPSSFVLTGIPGLESLSHVLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDAQLGQMFILHCFATVESGIFLAMAFAFDYVAIC
NPLRHSMLVLTYYVVGRLGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
40 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGTCASHLCAILIFYVP
IAVSSLIHRFGQCVPPPVTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
45 GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGTGTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA
ATGTTCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCTTGGCATGGCTTTTGA
50 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGTCACTTATACAGTGGTG
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGGTGTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCCTGCGGCTGCCCCCTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
55 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTATGTTCCCATGCTGTTTCTTCCCTGATTCACCG

ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

5 **AOLFR50 sequences:**

MNLDSSFFSLKSLIMALSNSSWRLPQPSFVLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYLFSLMLAAIDLVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILRLKLFQATHIGHAY
CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLKVPGNearLKAFST
10 CGSHVCVILVFYIPGMFSFLTHRFHHVPHHVHLLAJLYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

ATGAATTTGGATTCTTTTTTCTTTTCTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCCAGCCTTCTTTTTTCTGGTAGGAATTCCGGGTTTAGAGGAAAGC
15 CAGCACTGGATCGCACTGCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA
CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCTGTCC
ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCACTGC
TCCTGGTTCTGTGCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTACCCAT
GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
20 TTTGTCACCCCTTGCAACATCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
GGTGGTGTGGTGGGGGATTACTCTCTCATCCCCCTTCTCATTCTGTTGCGAAAACCTT
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG
25 GTACCAGGAAATGAGGCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
TCCTGGTCTTCTATATCCCGGGAATGTTCTCTTCTCACTCACCCTTGGTGCATGTA
CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTCACCTGCACTCAATCC
TCTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

30 **AOLFR51 sequences:**

MCQQLRDCILLIHLICNRKKVSLVMLGPAYNHTMETPASFLVLGIPGLQSSHLWLAIISLAM
YHALLGNTHIIVTAIWMDSTRHEPMYCFCLVLAADVIMASSVVPKMVSIFCSGSSISFSACFTQ
MFFVHLATAVETGLLLTMAFDRYVAICKPLHYKRILTPQVMLGMSMAITIRAIITPLSWMVS
HLPFCGSNVVVHSYCEHIALARLACADVPSSLYSLIGSSLMVGSDFVAFIAASYILILKAVFGLSS
35 KTAQLKALSTCGSHVGMALYYLPGMASIYAAWLQDQVPLHTQVLLADLYVIIPATLNPITY
GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
40 CTTCCTCCTTGTGGGTATCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTAGTGCTTGTTCCTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
45 CTGCTGTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTACATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
50 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAAGCATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCTTGACACCCCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
55 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISSLSAMYITALLGNTLIVTAIWMDSTRHEPMY
 CFLCVLAADVIVMASSVVPKMVSIFCSGDSSISFSACFTQMFFVHLATAVETGLLLTMAFDYRV
 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPFCSNVVVHVSCKHIALAR
 5 LACADVPVSSLYSLIGSSLMVGSVDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMALY
 YLPGMASIYAAWLQGDIVPLHTQVLLADLYVHIPATLNPITYGMRTKQLLEGIWSYLMHFLFDH
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCCTCCTTGTGGGTA
 10 TCCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTTAGGAAACACCTCATCGTGAAGTCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
 15 CTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA
 AGTGATGCTGGGAATGAGTATGGCCGTCAACCATCAGAGCTGTACATTTCATGACTCCACTG
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
 ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
 20 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCAAAGTGCTGCTAGCTGACCTGTACGT
 GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
 GGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ
 25 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
 LFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
 30 ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHITYCEHMGARLACA
 NITVNIVYGLTVALLAMGLDSILIAISYGFIHAFVHLP SHDAQHKALSTCGSHIGHILVFYIPAFF
 SFLTHRFHHEVPKHVHIFLANLYVLPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
 NO: 101)

ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
 35 CAGGGCTGGAGGCTGCCCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTGTAGC
 ACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT
 ATGTACCTCTTCTCTGCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC
 40 CAGATGTTTTGTGTCCATTCTATCTATGCTGTGGAGTCTCGATTCTACTTGCCATGGCCTT
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTTCTCAACCATGCTGTC
 ATAGGCAGAATTGGCTTTGTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
 CTTGCTGAGGCGACTCCCCACTGTGGTCACCGTGTCATGACACACACATACTGTGAGCAT
 ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
 45 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
 CATGCAGTCTTTCACCTTCCATCTCATGATGCCCAGCACAAAGCTCTGAGTACCTGTGGCT
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCTCCTCACCACCGC
 TTTGGTCACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTGCGAGTCGACT
 50 TCTAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKNIENVLCFVLFYIAIWMGNLLIMISITCTQ
 55 LIHQPMYFFLNYSLSLDCYTSTVTPKLMVDLLAERKTISYNNCMQLFTTHFFGGIEIFILTM
 AYDRYVAICKPLHYTHMSRQKCNTHIVCCTGGFIHSASQFLTIFVPFCGPNEIDHYFCDVYPLL
 KLACSNIHMIGLLVIANSGLIALVTFVLLLSYVFILYTIIRAYSAERRSKALATCSSHVIVVVLFF

APALFIYIRPVTTFSSEDKVFALFYTHIAPMFNPLIYTLRNTMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

5 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAGCAATAATA
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAAATAAGAACATTGAAGTCCTCTGCTTTGTA
TTATTTTGTGTTTGTACATTGCTATTTGGATGGGAACTTACTCATAATGATTTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
TTTGCTACACATCCACAGTGACCCCAAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
10 CATTTCCTATAATAACTGTATGATACAACCTCTTACCACCCATTTTTTTGGAGGCATAGAGA
TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTGTACCATTTTGTGGCCCAATGA
GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
TGATAGGTCTCTTAGTCATTGCTAATTGCTTAAATTGCTTTGGTGACATTTGTTGTCTTG
15 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA
AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCTGTTTTTGTCTCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTTGGCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTTGTTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
20 ID NO: 104)

AOLFR58 sequences:

MF SMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
25 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMC DLYLLELACTDTHIFGLMVVINSRG
FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

30 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTTACAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTTCTC
35 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA
TGCGTGCTTCTCATCTGTCATACCCCAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
40 GGCCTCTTGCAATTCCATGATACAAATTTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAATTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
45 TATTTGTATATACAGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAATATTA
AACTTTAA (SEQ ID NO: 106)

AOLFR59 sequences:

MGDWNNSDAVEPIFILRGFPGLLEYVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQP MYFYFI
SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILTNSVIGKIGLACLLRSLGVVLPTPLLLRHYHYCHGNALSHAFCLHQDVLRSLCTDA
RTNSIYGLCVVIATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS
55 MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLR RRF (SEQ ID NO:
107)

5 ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCCTG
 GACTGGAGTATGTTTCATTCTTGGCTCTCCATCCTCTTCTGTCTTGCATATTTGGTAGCATT
 ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
 10 TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCCACCA
 TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
 GTTCTTCATCCACACATTACATTCCCTGGAGTCCTCAGTGTGCTGGCCATGGCCTTTGACC
 GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCAACAGTGTAATTGGC
 AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGCTACT
 15 GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGACCAGGAT
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
 TTGCCACACTAGGTGTGGATTCAATCTTCTACTTCTTTCTTATGTTCTGATTCTTAATACT
 GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCAT
 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
 20 AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTTCCCCAGT
 CCTTAACCCTATTGTCTATAGTGTGAGAACAAGCAGATTCTGTCTAGGAATTCTCCACAAG
 TTTGTCCTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

20 MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
 MLATTDVGLSTATIPKMLGIFWINLRGIHFEACLTQMFFIHNFTLMESA VLVAMAYDSYVAICN
 PLQYSAILTNKVSVIGLGVFVRALIFVIPSILLILRPLFCGNHVIPHTYCEHMGHLSCASIKINI
 IYGLCAICNLVFDITVIALSYVHILCAVFRPLTHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
 25 FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKILLQEQQMEKEEYLIHTRF
 (SEQ ID NO: 109)

30 ATGTTCCCTTCCCAATGACACCCAGTTTACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
 ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
 ATAGGGAACTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCTACACCAGCCCATGT
 TCTACTTCCCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
 GATGCTTGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
 ATGTTTTTTATCCACAACCTTCACACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
 ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTTGT
 35 TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCAATCCCTCTATACTTC
 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCACAT
 GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
 TTTGTAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATCTTTGTGCT
 GTTTCCGTCTTCCCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTACATGT
 GTGTGTAATCCTTGCCCTTCTATACACCAGCCCTCTTTTCTTTATGACTCATTGCTTTGGCC
 40 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
 GCTCAATCCTGTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
 ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
 (SEQ ID NO: 110)

AOLFR61 sequences:

45 MSIINTSYVEITTFVLVGMPGLEIAHIWISIPICSMYLIAILNGNTILFIKTEPSLHGPMYYFLSML
 AMSDLGLSSLPTVLSIFLNPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT
 SILTTVRVAQIGIVFSFKSMMLLVLPFPFTLRLSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 50 GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYPILNLA VVHRFAG
 HVSPILNVL MANVLLLVPPLMKPIVYCVKTKQIRVRVVAKLQWKI (SEQ ID NO: 111)

55 ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCCATGT
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCCAT
 GTGTTAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCTGCTTTGCCACGGA

ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 GATTCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 5 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
 TGTGCAGTGATCATCTTCTACCTGCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG
 10 GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAAATGTTCTCTACTTGTACCTCCGCTGA
 TGAAACCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
 GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

MFYHNKSIFHPVTFFLIGIPGLEDFHMWISGPFCSVYL VALLGNATILLVIKVEQTLREPMFYFL
 15 AILSTIDLALSATSVPRMLGIFWFD AHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC
 APLHYATILTSVLVVGISMCI VIRPVLLTLP MVYLIYRLPFCQAHIIAHSYCEHMGIAKLSGNNIRI
 NGIYGLFVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
 HRFQHPGYIHILVANLYLIIPSLNPIHYGVR TKQIRERVLYVFTKK (SEQ ID NO: 113)

20 ATGTTTTATCACAAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTGGAATCCCAGG
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCTTTCTGCTCTGTTACCTTGTGGCTTTGC
 TGGGCAATGCCACCATCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
 CTACTTCTGGCCATTCTTTCCACTATTGATTGGCCCTTTCTGCAACCTCTGTGCCTCGCA
 TGCTGGGTATCTTCTGGTTTGATGCTCAGAGATTAACTATGGAGCTTGTGTGGCCAGAT
 25 GTTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT
 GGGCATTAGCATGTGCATTGTAATTCGTCCTGTTTACTTACACTTCCCATGGTCTATCTTA
 TCTACCGCTACCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
 CATTGCAAAATTGTCTGTGGAACATTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
 30 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
 TTCCGCCTCCCATCATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
 GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTTTCTTCTACTCATCGATTGGACAC
 CAAATACCAGGTTACATTCACATTCTTGTGGCAATCTCTATTTGATTATCCACCCCTCTCT
 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTCGAGAGCGAGTGTCTATGTTTTT
 35 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSINTSYVEITTFVLVGMPLGLE YAHIWISIPICSMYLIAILNGNTILFIKTEPSLHEPMYYFLSML
 40 AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQE FFIHGFSVLESSVLLIMSFDRLAIHNPLRYTS
 ILTTVRVAQIGIVFSFKSM LLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 GFFGALCLMVDFILIAVS YTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYPINLAVVHREFAR
 HVSPLINVL MANVLLLVPPLTNPIVYCVKTKQIRVRV VAKLCQRKI (SEQ ID NO: 115)

45 ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCCACT
 GTGTTAAGCATCTTCTGTTCAATGCTCCTGAAATTTTCATCCAATGCCTGCTTGTGCCAGGA
 ATTCTTCATTGATGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCTATTGATA
 50 GATTCCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 55 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
 TGTGCAGTGATCATCTTCTACCTGCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG

GCATGTCTCTCCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCAATTGTTTATTGTGTAATAAAGATAAGAGTGAGAGTTGTAGCAAAATT
GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

5 AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTIVLGNLTILHVICTDATLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
HDSTVLTPACIVKMGLSSVLRALLILPLPFLKRFQYCHSHVLAHA YCLHLEIMKLACSSIIVN
HIYGLFVVA CTVGVDLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
10 HRFGEHLPRVVHLFMSYVYLLVPPLMNPPIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG
GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
15 TTGGGGAACCTCACCATTCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGT
ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCACT
GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGACACCTGCATGTATTG
20 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCTTGGCATTCTCT
CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTACCTGGA
GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG
GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC
CGTGCTCAGCATTGCCTCCACAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
25 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTGTGCATCGCTTTGG
TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCCTATGTGTATCTGCTGGTACCACCCC
TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTGCCAGCGCATCATTAAAGAA
GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

30 AOLFR65 sequences:

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPFFVYLVALLGNTALLFVIQTEQSLHEPM
YYFLAMLDSIDLGLSTATIPKMLGIFWNTKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYI
AICKPLRYTMILTSKIIISLIAGI AVLRSLYMVVPLVFLRLPFCGHRIIPHTYCEHMGRIARLACAS
IKVNIRFGLGNISLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
35 THRFHGNIPQYIHILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCCTACTGCT
GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTAT
CTTGTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC
40 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTGGAGGC
TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
CATGGCCTTTGACCGCTACATTGCCATTGCAACCTCTTCGGTACACCATGATCCTCACCA
GCAAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTCC
45 ACTGGTGTTTCTCCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT
GTGAGCACATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
CCTTGGCAACATATCTCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTCAGGA
TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
GGTTCTCATATTGGTGTTATCTTAGCCTTTTTTACACCAGCATTTTTTTCATTCTTGACACA
50 TCGTTTTGGCCATAATATCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG
TCCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTCGAGAGAGAG
TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

55 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDALHRPMYVFL
ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMMLMALDHCVAI

CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
VRVNAIYGLIVALLIGGFIDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
TFFTHHFGGHTIPLHHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
ID NO: 121)

5

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTTCATCCTAAATGGCATCCCTG
GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
ATGTCCTTCCTTGCCCTTCTTTCCCTTCACAGATGTGCTCATGTGCACCAGCACCCTTCCCAAC
10 ACTCTCTTCATATTGTGGTTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT
GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAAGTCATTGC
TAAAGCTGGGTTCCTCACTTTTCTTAGGGGTGTGATGCTTGTTATCCCTTCCACTTTCTCTCA
CCAAGCGCCTTCCATACTGCAAGGGCAACGTACATACCCACACCTACTGTGACCACATGTC
15 TGTGGCCAAGATATCTTGTGTAATGTGAGGGTTAACGCCATCTATGGTTTGATAGTTGCC
CTGCTGATTGGGGGCTTTGATATCCTGTGCAATACAACTCTCTACACTATGATTCTTCAAGC
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACCTGCCAC
TTCTGTGCCATAGTCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCACTTTTGG
GGGACACACCATTCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
20 CCACAATGAACCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAGTGTCAATTA
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYILAVVGNCGLICISHEEALHRPMPYYFLA
25 LLSFTDVTLCCTTMVPMNMLCIFWNLKEIDFNACLAQMFFVHMLTGMESGVLMLMALDRYVAI
CYPLRYATILTNPVIAKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
FKVNAIYGLMVALLIGVFDICISVSYTMILQAVMSLSSADARHKAFTSTCTSHMCSIVITYVAAF
FTFFTHRFVGHNPNIHIIIVANLYLLPPTMNPVYGVKTKQIQEGVIKFLLGDKVSFTYDK
(SEQ ID NO: 123)

30

ATGTCTGGGGACAACAGCTCCAGCCTGACCCCAGGATTCTTTATCTTGAATGGCGTTCTTG
GGCTGGAAGCCACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
GTGGGGAACCTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTCACCTTGTGCACCACCATGGTACCTAAT
35 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCAGA
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCACTCTCCTC
ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCCACACCTACTGTGACCATATGT
40 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTCACCTTTTTTCACTCATCGTTTTGT
AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
45 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTCAGGAAGGTGTAATTA
AATTTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTTLLMTIWLLEASLHQPL
50 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMESCTFMVMA YDRY
VAICHPLRYPSTIDHFVVKAAFILTRNVLMTLPIPLSAQLRYCGRNVIENCICANMSVSR LSC
DDVTINHL YQFAGGWTL LGSDDLIFLSYTFILRAVLR LKAEGAVAKALSTCGSHFMLILFFSTIL
LVFVLTHVAKKKVSPDVPVLLNVLHHVIPALNP IYGVRTQEIKQGMQRLLKKGC (SEQ ID
NO: 125)

55

ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
TTGTGAGATCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCCCAGCCTCCTTTTCCTCTTG
GCCGTAGGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
5 CCCAAGGTCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCCT
CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTTCATGGTCATGGCC
TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT
TGATGTCAAGGCTGCCATGTTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
ATCCTTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
10 ATATGCTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCCTCTCCTACACCTTCATTCT
GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
CTCCCACTTCATGCTCATCCTCTTCTTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT
GGCTAAGAAGAAAGTCTCCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCAAT
15 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCCAAAGAAATTAAGCAGGGAATG
CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKVLDFNMKNVTEVTLFVLKGFTDNLELQ
20 TIFFFLFLAIYLTLMGNLGLILVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYMLINASYVAGI
LHATHITVATFSLFCGANEIRRVFC DIPPLAISYSDHTNQLLLFYFVGSIELVTILIVLISYGLIL
LAILKMYSAEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV
IYSLRNKDVKDSMKKMFGKNQVINKVYFHTKK (SEQ ID NO: 127)

ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCCTGAGTCATGGTGTGTTTCATT
CTTTTTGTCATAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC
ATGAAGAATGTCACTGAAGTTACCTTATTTGACTGAAGGGCTTCACAGACAATCTTGAAC
TGCAGACTATCTTCTTCTTCTGTTTCTAGCAATCTACCTCTTCACTCTCAGGGAAATTA
30 GGACTGATTTTAGTGGTCATTAGGGATTCCAGCTCCACAAACCCATGTACTATTTCTGA
GTATGTTGTCTTCTGTGGATGCCTGCTATTCTCAGTTATTACCCCAAATATGTTAGTAGAT
TTTACGACAAAGAATAAAGTCATTTCACTTCTTGGATGTGTAGCACAGGTGTTTCTTGCTT
GTAGTTTTGGAACCAAGAAATGCTTTCTTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
CATCTACAACCCCTCTCCTGTATTCACTGAGCATGTCAACCCAGAGTCTACATGCCACTCATC
35 AATGCTTCTTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCCTCTCCTTGCTA
TTTCTTATTCTGACACTCACACAAACCAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTTGATTCTGTTGGCCATTCTGAAGAT
GTATTCTGCTGAAGGGAGGAGAAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
40 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCAGCTATGCTCG
GACCATGACATGATAGTGTCAATATTTTACACCATGTGATTCCCTTGCTGAATCCCGTCAT
CTACAGTTTGAGGAACAAAGATGTAAAGACTCAATGAAAAAAATGTTTGGGAAAAATCA
GGTTATCAATAAAGTATATTTTCACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

MDSTFTGYNLVNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
YLFTLIGNLGLVVLVIEDSWLHNP MY YFLSVLSFLDACYSTV VTPKMLVNFLAKNKSISFIGCA
TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASVYVAGILHATHIVA
TFSLSFCGSNEIRHVFCMPPLAISCS DHTNQLLLFYFVGSIEIVTILIVLISCDFILLSILKMHS
50 KGRQKAFSTCGSHLTGVTIYHGTILVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIYSLRNKEVK
KAVKKMLKL VYK (SEQ ID NO: 129)

ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAAAGTGAATGGACA
AGTTGTATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
55 TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCTATTTTACTATTT
TTTGAATCTATCTCTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG

ATTCTGGCTCCACAACCCCATGTATTATTTCTTAGTGTTTTATCATTCTTGGATGCTTGC
TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAATCCATTT
CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT
CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCTCTCCTGTATTCACT
5 GAGCATGTCACCCAGAGTCTATGTGCCACTCATCACTGCTTCTACGTTGCTGGCATTTTAC
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG
GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGCTCCTCATT
TCTGTGATTTTCATTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
10 CCTTCTCTACATGTGGCTCTCAGCTAAGTGGAGTGACAATTTATCATGGAACAATTCTCGTC
AGTTATATGAGACCAAGTTCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

15 **AOLFR71 sequences:**

MGRNNTNVPDFILTGLSDSEEVQMALFILFLIYITMLGNVGMILIRLDLQLHTPMYFFLTH
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPLRY
PVMISKRLLCCALVTGPYVISFINSFVNVWMSRLHFCDNSNVVRHFFCDTSPILALSCMDTYDIEI
MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLPKPRK
20 SYSLGRDQVASVFYITIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
AATGTGGGGATGATATTGATAATCCGCTGGACCTCCAGCTTCACACTCCCATGTATTTTT
25 TCCTTACTCACTTGTCAATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAACCTTA
GCGAACTTACTGACTTCCAATATATTTCTTTCATGGGCTGCTTTGCCAGATGTTCTTTTT
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG
CTATCTGCAGTCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTG
ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
30 TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTCTGCGACACGTCTCCAATTTTAGCT
CTGTCTGCTGATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCTGAAA
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG
TCACCATCTTTTATGGAAGTATGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
35 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCAGTGAATCCACTCAT
TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
GGACTCCAGGTAA (SEQ ID NO: 132)

AOLFR72 sequences:

40 MAPENFTRVTEFILTVSSCELPQLPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
ALINLGNSTVIAPKMLINFLVKKKTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
YMVVVSRRLCLLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFCYCDNVPLLALSCSDTYLPE
TVVFISAATNVVGSLLIIVLSYFNVLSILKICSSEGRKKAFTSCASHMMAVTIFYGTLLFMYVQP
RSNHSLDTDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:
45 133)

ATGGCTCCTGAAAAATTCACCAAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG
GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
50 TCCTGCAACATCTGGCTCTCATTAACTTTGGTAACTCTACTGTCAATGCCCCATAAATGCTG
ATTAATTTTTAGTAAAGAAGAAAACCTCATTCTATGAATGTGCCACCCAACTGGGAG
GGTCTTGTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
55 CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA

ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
CAGTCACAATTTTTTATGGGACATTGCTATTCATGTATGTGCAGCCCCGAAGTAACCATTC
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT
5 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
AATCTGTGCTATTCCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

10 MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFGFLFIYLVTVIGNLGMVILTYLDSKLHTP
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIHSELFILSAMAYDRYV
AICKPLLYVIIMAELVWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL
QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

15 ATGAATCATGTGGTAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA
TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
CACACCCCATGTACTTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
CATTGCCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
20 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
TCTCACAATTAAGTTATTTAACTGTCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT
GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
25 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTACTTGCA
ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTATACCCTGTTG
ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA
30 AGAGAACTTTAACCAATCGATTCAAAATTCCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFAFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
LAFMDLGYSTTVGPKMLVNFVVDKNIISYFYCATQLAFFLVFIGSELFILSAMSVDLYVAICNPL
35 LYTVIMSRRCQVLVAIPYLYCTFISLLVTIKIFTLSCGYNVISHFYCDSLPLPLLCNTHIEILI
ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH
SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

40 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
GCAATTTGGGCATGATTGTCTCACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT
TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACGTGGGACCCAAAATG
TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
45 TTTCTTTCTTGTGTTTATTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCCTACGACCTCT
ATGTGGCCATCTGTAAACCTCTGCTATACACAGTAATCATGTCACGAAGGGTATGTCAGGT
GCTGGTAGCAATCCCTTACCTCTATTGCACATTTCATTCTCTTCTAGTCACCATAAAGATT
TTACTTTATCCTTCTGTGGCTACAACGCTATTAGTCATTTCTACTGTGACAGTCTCCCTTTG
TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT
TGATTGATTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
50 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTTCTACCTGTGGAGCCCACCTGACAGTG
GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCCT
TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCATGTTGAATCCCTTGA
TCTATAGTTTACGAAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAAATTATG
TAATATTTTGTTTAA (SEQ ID NO: 138)

55

AOLFR75 sequences:

MEGKNQTNISEFLLGFSSWQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNQITQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 CHPLHYSTIMALRLCASLVAAPWVIAILNPLHLTMMMAHLHFCSDNVIIHFFCDINSLPLSCSD
 5 TSLNQLSVLATVGLIFVVPVCILVSYLIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYSLRNNELKGTLLKTLSPRGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 10 AACACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTTAACAGGGCTGTTTGGA
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 CTGTATGATGTTTGCCAATATGGACAATTTCTTCTCACAGTGATGGCATATGACCGTTAC
 15 GTGGCCATCTGTCACCCCTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT
 GGTAGCTGCACCTTGGGTCAATTGCCATTTTGAACCTCTCTTGACACTCTTATGATGGCCC
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCTGTTCGACACCACTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA
 TCTTTGTGGTACCTTCACTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
 20 AAAGTCCCTTCTGCCCCAAGGAAAACCAAGGCTTCTCTACCTGTGGATCTCACCTTGCCTT
 GGTCACTCTTTTCTATGGAGCAAAACACAGGGGTCTATATGAGCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTTATGGTTGTAGCACCTGTGTTGAATCCAT
 TCATTTACAGTTTAAGAAACAATGAAGTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
 CGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 25 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLTITLGNLGMIIILLDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLTLGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 30 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
 VLISSFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFTMIIPMLSPIVYTLRNDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 35 CTACAGGTTCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTTGT
 GCACTCTTTGCCACTGTGGAAAATTACCTCTTGCTCCTCAATGGCCTATGACCGCTACGCAG
 40 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTCGCC
 TCTCTTTCTGCATGTCCAATGTGATTTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTTAATGT
 CTTTTTGCACCTCTTGTACCTTGATTTCTATCTGTTTCATATTGATCACCATTTCTTAAGAG
 45 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT
 50 ATTCTCTAGATTCACTCTTTTAA (SEQ ID NO: 142)

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVLMSYDRYVAVC
 QPLQYPVLMRRQVCLLMMGSSWVVGVLNASIQTSITLHFPYCASRIVDHFCEVPALLKLSCA
 55 DTCA YEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGLFYGA

AVFMYMVPCAYHSPQQDNVVSFLFYSLVTPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
(SEQ ID NO: 143)

5 ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTATGTTTGTATAGGCCTTCTGGGC
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCCT
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
10 TCCTCACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA
TGTTGCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCCTCCTGGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC
TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
15 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCACCACCTGCTCCTCGCACATCA
CGGTAGTGGGGCTCTTTTATGGTGCCGCGCTGTTTATGTACATGGTGCCTTGCAGCTACCA
CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTACCCCTACACTCAAC
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

20

AOLFR78 sequences:

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFLGASEFLLAVMSADRYLAICH
PLRYPLMSGAVCFRVALACWVGGLVPVLGPTVAVALLPFCQKQAVVQHFFCDSGPLRLRLAC
25 TNTKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
FLYVRPSQSGSVDTNWAVTVITTFVTPLLNPFYIALRNEQVKEALKDMFRKVVAGVLGNLLLD
KCLSEKAVK (SEQ ID NO: 145)

30 ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT
GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
GTACTTCTTTCTGGGTAACCTGTCTGCCTAGAGATACTGCTCACTTCTGTCTATCTCCAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCATGTATCACCCA
ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGTCTGTCTGCGG
35 ATCGCTACCTGGCCATCTGTATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG
CTTTCTGTGTGGCCTTGCCCTGCTGGGTGGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG
GCTGTGGCCTTGCTTCTCTTTCTGTAAGCAGGGTGTGTGGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCCTGGCTTGCACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CCTGGCCTCCCTCGTCATTGTATCTTCTTGTGATCACTGCTGTGTCTACGGCCTCATTG
40 TGCTGGCAGTCTGAGCATCCCCTCTGCTTCAGGCCGTGAGAAGGCCTTCTCTACCTGTAC
CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTGTGACAC
CACTGTTGAATCCATTCTATGCCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT
45 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMALIFTDSHLQSP
MYFFLNVL SFLDICYSSVTPKLLVNFLVSDKISFEGCVVQLAFFVHVTAESFLLASMA YDR
50 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAIQTGNVFALPFCGPNQLTHYYCDIPLLH
LACANTATARVVLYVFSALVTLLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSFYTHIIPMLNPFYISLRNKEVKGALQKQLQVNIFFG
(SEQ ID NO: 147)

55 ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCCAAGTTCATCT
TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTTCTCGGAGCCATCCTGCTCAT

SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, 5 SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, 10 SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, 15 SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, 20 SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

- 25 21. The method of Claim 20, wherein the ligand is a primary odorant.
22. A compound which blocks activation of an olfactory receptor identified by Claim 20.

NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID
NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID
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5 NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
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NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID
10 NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ
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15 NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151,
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SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID
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 5 SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID
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 15 SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID
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 NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
 511.

20

19. A primary odorant identified by Claim 18.
20. A method of identifying a compound which blocks activation by a odorant of
 at least one olfactory receptor comprising:
 - 25 (a) producing a structurally-related candidate compound from a ligand of
 the at least one olfactory receptor,
 - (b) measuring activation by the odorant of the at least one olfactory
 receptor with the candidate compound, and
 - (c) identifying the candidate compound as a compound which blocks
 30 activation if activation of the at least one olfactory receptor is reduced or
 inhibited;

wherein at least one of the olfactory receptors has an amino acid sequence selected
 from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID

NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID
NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID
NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID
5 NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID
NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ
ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115,
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NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133,
10 SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID
NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151,
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SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID
25 NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,
SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID
NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295,
SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID
NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313,
30 SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID
NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331,
SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID
NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349,

- 5 (a) measuring values X_1 to X_n representative of at least one activity selected from the group consisting of binding a desirable odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with a desirable odorant, and blocking at least one of n olfactory receptors with a desirable odorant;
- (b) generating a representation of the desirable odorant from the values X_1 to X_n ;
- 10 (c) decomposing the desirable odorant's representation into representations of known odorants from the database of Claim 14 or superposing known odorants' representations from the database to reproduce the desirable odorant; and
- (d) formulating the known odorants to reproduce sensory perception of the desirable odorant and thereby produce the artificial odorant.

15 17. An artificial odorant produced by Claim 16.

18. A method of identifying a primary odorant related to sensory perception comprising:

- 20 (a) providing a representative class of n olfactory receptors or ligand-binding domains thereof,
- (b) measuring at least one activity of a odorant selected from the group consisting of binding of the candidate odorant to the ligand-binding domain of at least one of the n olfactory receptors and activating with the candidate odorant at least one of the n olfactory receptors, and
- 25 (c) identifying the candidate odorant as a primary odorant if only one or less than 10% of the representative class of n olfactory receptors is bound or activated;

wherein at least one of the n olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID

9. The method of Claim 1, wherein the value measured for activating an olfactory receptor is above a preset limit for specific activation.
10. The method of Claim 1, wherein the value measured for blocking an olfactory
5 receptor is at least a reduction in binding of the odorant or activation by the odorant.
11. The method of Claim 1, wherein the representation of sensory perception is generated with a neural network.
- 10 12. A biosensor comprised of the n ligand-binding domains or olfactory receptors of Claim 1.
13. A method for producing a database of odorant representations comprising:
15 (a) providing one or more known odorants and
(b) generating a representation of the one or more known odorants in accordance with the method of Claim 1 to produce the database.
14. A database produced by Claim 13.
- 20 15. A method of identifying an unknown odorant comprising:
(a) measuring values X_1 to X_n representative of at least one activity selected from the group consisting of binding the unknown odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with the unknown odorant, and blocking at
25 least one of n olfactory receptors with the unknown odorant;
(b) generating a representation of the unknown odorant from the values X_1 to X_n ; and
(c) comparing the unknown odorant's representation to the database of Claim 14 to identify the known odorant which is most similar in
30 representation.
16. A method of producing an artificial odorant comprising:

NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475,
SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID
NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493,
SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID
5 NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
511.

2. The method of Claim 1, wherein at least one of the olfactory receptors
specifically recognizes the odorant, and there are between 5 and 350 of the n olfactory
10 receptors selected from the listed amino acid sequences.

3. The method of Claim 1, wherein at least two different activities are measured
to provide the values X_1 to X_n .

15 4. The method of Claim 1, wherein each odorant receptor is expressed in cells,
and the cells expressing each odorant receptor are located at an identifiable position.

5. The method of Claim 1, wherein at least one olfactory receptor is soluble, and
binding of odorant to a ligand-binding domain of the soluble olfactory receptor is
20 measured in solution.

6. The method of Claim 1, wherein at least one olfactory receptor is in solid state,
and binding of odorant to a ligand-binding domain of the solid-state olfactory receptor
is measured on a substrate.
25

7. The method of Claim 1, wherein the value measured for binding is above a
preset limit for specific binding to olfactory receptors.

8. – The method of Claim 1, wherein the value measured for activating an olfactory
30 receptor is derived from a signal selected from the group consisting of intracellular
 Ca^{2+} , cAMP, cGMP and IP3.

SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID
NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187,
SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID
NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205,
5 SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID
NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223,
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NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241,
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10 NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259,
SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID
NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,
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15 SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID
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NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385,
25 SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID
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SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID
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30 NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439,
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SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID

Claims:

1. A method for representing sensory perception of one or more odorants comprising:
 - 5 (a) providing a representative class of n olfactory receptors or ligand-binding domains thereof;
 - (b) measuring values X_1 to X_n representative of at least one activity of the one or more odorants selected from the group consisting of binding of the one or more odorants to the ligand-binding domain of at least one of the n
 - 10 olfactory receptors, activating at least one of the n olfactory receptors with the one or more odorants, and blocking at least one of the n olfactory receptors with the one or more odorants; and
 - (c) generating a representation of sensory perception from the values X_1 to X_n ;
- 15 wherein at least one of the n olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133,
 - 20 SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169,
 - 25
 - 30

TGTTCTTCATCCATTTCTTCACTGTTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
GCCTCATTGCAGGCATTGCTGTCCTGAGGAGCTTGACATGGTCATTCCACTGGTGTTTCT
CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
5 GCATTGCCCCGCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
TTCTCTCTTGTTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
GGTGTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT
GATATTCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCCTCCACCCT
10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

MALGNHSTITEFLLGLSADPNIRALLFVLFLGIYLLTIMENLMLLLVIRADSCLHKPMYFFLSH
15 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
LLYGQIMGKQLYMHVLVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI
SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTISISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGGATTACCTCCTGACCATAATGGA
AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAGTCATTGTGCCCCAAGATGCTG
GAGAACCTCCTGTACAGAGGAAAACCATTTTCAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
TGCTGCCATCCGCCGCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCCTCCTAGCTG
TAAACATGGTCTTTTGTGAAGCCAAAATCATTCAACCACTACAGCTATGAGATGCCATCCCT
CCTCCCTCTGTCCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC
30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA
CTGCAGTGACACTTTACTATGGCTCAGGTTTGCTCCGCCATCTCATGCCAAACTCAGGTTT
CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCCTCA
TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT
35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)

NELVLFTVFGFIELSTISGVFISYCYILSVLEIHSAGRFKALSTCTSHLSAVAI FQGTL LFM YFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAA AATTGCTCCTCATTA AACTGATTTT TTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTATATCATTAATTTCTCAGCAA
ATCTTGAATGATAGTTTTAATCAGAATGGATTGACCAACTTACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTGCTAGTGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTTATTCACCGTCTTTGGTTTTA
TTGAACTGAGTACCATTTTCAGGAGTTTTCATTTCTTATTGTTATATCATCCTATCAGTCTTG
15 GAGATCACTCTGCTGAGGGGAGGTTCAAAGCTCTCTCTACATGCACTTCCCACTTATCTG
CGTTTGCAATTTTCCAGGGAACCTGCTCTTTATGTATTTCCGGCCAAGTTCTTCCCTATTCT
CTAGATCAAGATAAAAATGACCTCATTTGTTTTACACCCTTGTGGTTCCCATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFHFGLSGIECFLFTVMA YDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL
AQRVSFTNVGLISLVCFLILLISYTRITISILSIRTTEGRRRAFSTCSAHLIAILCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCCACACACA
30 GAGGGGCTGGAGATGACACTTTTGTCTTATTCTGCCCTTCTATGCCTGCACTCTACTGGG
AAATGTGTCTATCCTTGTTGCTGTTATGTCTTCTGCTCGCCTTCACACACTATGTATTTCT
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTTCTCCTCAGTGACTGTGTCCCAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC
35 ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
TGGCTGTGGGCACATGGCTGTTAGGGTGCATTCAATCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTTTGTCTGCTTTCTGCTAATTCTTTTATCCTACACTAGAATCACAATATCTATCTT
40 AAGCATTTCGTACAACATGAGGCGCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT
GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCATGAATCTGGTAGGACCAATGCTGAACCTTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

50 MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVQTEQSLHEPMYYCLA
MLDSIDLSLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGIAVLRSLYMVPLVFLLLRLPFCGHRIPHTYCEHMGARLACASIKVNM
FGLGSISLLLLDVLILILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
DIPQYIHIFLANLYVVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

55 ATGCCTATAGCTAACGACACCCAGTTCCTACTTCTTCATTCTCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTCTCTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAAACTGAGCAGAGTCTCCATGAGCCCCATGA
CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCCAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTGGAGGCTACCTTTCTCAGA

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
 CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
 TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
 AAACCTTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
 VVPHILANTLQSEKTTLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLLMTLTL
 CVHLVVASVISGLFSLQLVAFISLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
 10 AIAVPFLLITTSYTFIVAALLKIHSAAGRHRAPSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
 DRFISLVYTLGTPLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTGCTGGCCTATCCCTCCTGCCCAGAACTGCATATTCTGTCCTTCCTTGG
 GGTGAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTACAC
 15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGCGGCAGCCTTTCTGGGATTGAAA
 TATGCTACACTGCAGTGGTGGTGGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
 CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGCTGAT
 TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA
 CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
 20 TGTTCTCTGTCCTTACAACTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC
 ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT
 TCATGAGCAGTCAGTGCTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
 ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
 ACCGGGCCTTCTCCACCTGCTCTTCCCACCTCACTGTGGTGTGCTGCTGCAGTATGGCTGCTGT
 25 GCCTTCATGACATGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
 TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA
 GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAAGTGCCTTTCCCAGAACAGCTAG
 (SEQ ID NO: 502)

30 **AOLFR276B sequences:**

MGGFGTNISSSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIKEEQSLHQPMYYFLS
 LFSVNDLGVFSFTLPTVLAAVCFHAPETTFDCLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP
 LRYATVLTVDVRVAHNGISIVRSFCMVFLPLPFLKRLPFCKASVVLHASYCLHADLRLPWGDT
 TINSYGLFVISAAGVDSLLILLSYVLILHVSVAIASRGERLKTNLNTCVSHIYAVLIFYVPMVSVS
 35 MVHFRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCCTCCCTG
 AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCTT
 40 CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGACCAGCCAATG
 TACTACTTCTGTCTCTTTTTCTGTAAATGACCTGGGTGTGCTCTTTCTACATTGCCCACT
 GTACTGGCTGCTGTGTGTTTTATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCGAGA
 TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTGTAC
 CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
 CCCACAATGGCATATCCATTGTCATCCGAGCTTCTGCATGGTATTCCCACTTCCCTTCTC
 45 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCCTACTGTCTGCATG
 CAGACCTGATTTCGGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTAT
 TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC
 ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
 ACATATCTATGCAGTGCTGATCTTCTATGTGCCTATGGTTAGTGTGTCCATGGTTCATCGAT
 50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
 ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINFSANLGMIVLIRMDYQLHTPMYFFLS
 55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDRYKAJINP
 LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTTAC
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 5 GCCTGTGCTGGTATCATGTTTCATTTCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC
 ATTTCTGCCATCCTGAGGATGCATTGAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMA YDCYVAICSPL
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINHFYCDLFLALSCSDTHMK
 EILIFAFAGFDMISSSSIVLTSYIFIIAILRIRSTQGQHKAI STCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILTFLKIRKLY (SEQ
 ID NO: 497)

ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCATTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTGGAACGCAACACCATTCTTTCCATGCTTGTGCAACCCAACTGGGTT
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTTCTATTGTGATGACCTCCCCCTTCTT
 AGCTCTGTCTGCTCAGACACACATGAAGGAAATTCTGATATTTGCCCTTGTGCTGGCCTT
 30 GATATGATCTCTTCTCTTCCATTGCTCCTCACCTCCTACATCTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 35 GTTGTGAAAACCTACAGATATTAACATTTTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFIFLTYMLNGLNLTITLTLDDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRFLTSMITTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYCDYGPLVELACSDTSLELMVI
 LLAVVTLMTLVTLVTLSTYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE
 GGAFNKGI AVLITSVTPLNPFYITLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTTCTCACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCCG
 GAATTTCTCCTTCTTAGAAATTTCTTTCACATCCATTTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTGTCTAT
 50 ATTTCTTGGAGCTACCGAGTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACCTAGTGTT
 CTGCTCCTGGTTGGGGGGATTCTTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT
 TGCCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCTCCACATGATTGTCTATC

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
 TCCAGGTGGCAGTTTTACCTTTCTTTTCTTGCATTTTACTCAGCATCCTTGGAAATCTG
 ACTATCCTCATCCTCACCTTGCTGGACTCCACCTTCAGACTCCCATGTATTTCTTTCTCCG
 5 GAACTTCTCCTTCTTGGAAATTTCTTTCACAAACATCTTCATTCCAAGGGTCTGATTAGCA
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
 GTTCCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
 CTCTCATGTTTACAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCATTATCAAGACTATTCTGAAG
 CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTCAT
 CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
 15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
 TTACACCCTAAGGAACCAACAGGTAAAACAACCCCTTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
 ALIDICYTTTNPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHPFCGNNQINYYFFCDIPLLILSCGDTSLNE
 LALLSIGILISWTPFLCIILSYLYIISTILRJSSEGRHKAFTSCASHLLIVILYYGSAIFTYVRPISSYS
 LEKDRLLISVLVSVPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTTCGACCACCTGA
 ATGAATTGCAGTATTTACTCTTACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTTCCACCTACACACACCCATGTATTATTT
 CCTAGGAAATCTTGGCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
 30 GTGCATCTTCTGTGAGAGAAGAAATCAATTTCTATGGAGGCTGTGTGACCCAGCTCTTTG
 GTTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC
 ATAAGCTGGACTCCTTTCTGTGCATCATCCTTTCTACCTTTACATCATCTCCACCATCCT
 GAGGATCCGTTCTCTGAGGGGAGGGCACAAGCCTTTTCCACCTGTGCCTCCCACCTGCTC
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGCACACCCATGCTGAATCCT
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGCCACCAGTTTTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFLSIYLFVVGNLGLILLIRADTSLNTPM
 YFFLSNLAFFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAFYDRY
 VAICNPLLYMVVMTPGICQLVAVPYSYFLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL
 TCSDFRFLQWIFACAGIMFISSLLIVFVSYMFIIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
 TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKVEKALKKIIHNKN (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCCTCTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGTACTCTACTCATTAGAGCGGATACAAGTCTCAACA
 CACCAATGTACTTCTTCTTAGCACTAGCTTTTGTGGATTCTGTGTTACTCTTCTGTGCTATT
 55 ACACCCAAAATGCTTGGGAATTTCTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
 CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

AOLFR24B sequences:

MPSINDTHFYPPFLLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
 LQYTMILTINKTISILASVVVGRNLVLVTPFVFLRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
 5 IYGLMVISYIIVDVILLASSYVLILRAVFLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
 RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCTCCTGCTAGGAATACCAGG
 ACTGGACACTTTACATATCTGGATTTCTTTCCCATTCTGTATTGTGTACCTGATTGCCATTG
 10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
 CTACTTCCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
 TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
 GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
 GCTTTGTTGCCATCTGCAACCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
 15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA
 TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
 TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
 TCTTATATTATTGTGGATGTGATCTTAATTGCCTTTCCTATGTGCTTATCCTTAGAGCTGT
 TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT
 20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTTCTTTTATGACACATCGTTTTGGCCAA
 AACATTCCCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCACCTGCCCT
 TAACCCTGTCATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
 GTACAGAAAGAATAA (SEQ ID NO: 488)

25 **AOLFR33B sequences:**

MLHTNNTQFHPSTFLVVGVPGLVDVHVWIGFPFAVYLTALLGNIILFVIQTEQSLHQPMFYFL
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTHICTGLESVVLTVTGIDRYIAICNP
 LRYSMILTINKVIAILGIVIVRTL VFVTPFTFLTLRLPFCGVRIIPHTYCEHMGLAKLACASINVTY
 30 GLIAFSVGYIDISVIGFSYVQILRAVFHLPWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF
 GHNPYHYIHILLANLYVVFPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
 (SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTACCCTTCCACCTTCTCGTAGTGCGGGTCCCAG
 GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
 35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
 TTTTACTTCCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
 AGATGCTGGGAATTTTCTGGTTTAATCTTGAGAGATTGCATTTGGTGCCTGCATCACACA
 GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
 GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
 40 TAGCCATTCTGGGCATAGTCATCATTGTCAGGACTTTGGTATTTGTGACTCCATTCACATTT
 CTCACCCTGAGATTGCCCTTTCTGTGGTGTCCGATTATCCCTCATACCTATTGTGAACACAT
 GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCCTTCTCA
 GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT
 CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCGTG
 45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCTTCATGACACACCGCTTTGGCCACAA
 CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCCTGCTCTTA
 ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
 ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTAGTTAGACA
 50 ATAA (SEQ ID NO: 490)

55 **AOLFR112B sequences:**

MKNKTVLTFEILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLLDSDLQTPMYFFLRNFSF
 LEISFTNIFIPRVLISITTNKNSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
 MSSRICIQLIFCSWLGLMAIPTITLMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVFL
 55 VASVTLVVTLLVLVLSYAFIILKLPKSAQRTKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG
 DTFNKGVALLITSVAPLLNPFYTLRNQVQVKQPFKDMVKLLNL (SEQ ID NO: 491)

GAGGATCCAGTAATGGGGAGGGCCGAGACCGACTTACTCTTCCTGCTCCTTCCACCTTT
GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTG
5 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

MESNQTWITEVILLGFQVDPALELFLFGFLLFYSLTLMGNGIILGLIYLDLRLHTPMYVFLSHL
AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFAITECLILVMMCYDRYVAICHPL
10 QYTLIMNWRVCTVLAFTWIFSLALVHITLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN
QVVLFAFSFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPLNPLIYSLRNAEVLKALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
15 GCTCTGGAGTTGTTCTCTTTGGGTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAATCTTGATGCACAAAAAGTCATCTCCTTTGCTCCTTGCTACTTCAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTCACCCCTTGCAATACACCTCATTATGAACTGGAGAGTGTGCACTGTCTT
GGCTCAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTTGTGGCCCAAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTTATTTGCGGGTCTGCGTTCA
TCTTAGTGGGGCCGCTCTGCCTGGTGTCTCCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGAGAAAGCCCTTCTCTACCTGCTCCTCCACCTCTGCG
TGGTGGGGCTTTCTTTGGCAGCGCCATTGTCTCATGTACATGGCCCCCAAGTCAAGCCATTC
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCTTTGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

30

AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPLRLTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVMSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
35 EIFVAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFSTCSSHL CVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNPLNPLIYSLRNAQVKALYRALQKKRTM (SEQ ID NO:
485).

ATGGGGGACAACCAATCACGGGTACAGAAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTTTCAGCCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAACACAAAAAACTATCTCGTTCATCTCTTGCAATTATGCAGATGGCTTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT
45 GGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTTCTGTCTCTCCTC
AACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTTG
TCTTAGTCGGGGCCCCTTCTCTGATGCTCATCTCCTACATGCGCATCCTCTTGGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTTTCCACCTGCTCCTCCACCTCTGTG
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATTCTCACCCCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
CTGTAACCCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
CTTACTGTGGCTCCCGAAGTATCAACCATTTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
5 GGCCTGTGCAGACAGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGTCTCATGTTG
CTCATCCCCATCTCTATCATCTCCACTTCTACTCCCTCATCTTGTTAACCATCCACCGCAT
GCCCTCTGCTGAAGGTCGAAAAAGGCCTTCACCACTTGTTCCTCCCACTTGACTGTAGTT
AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTCCACACCCCCG
AGCAGGACAAAGTAGTGTGACGCTTCTATACCATTGTCACGCCCATGCTTAATCCTCTCAT
10 CTACAGCCTCAGAAACAAGGACGTATAGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA
TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSLRHTPMYFLLSQLS
15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYTLAGAEEFLLGLMSYDRYVAICNPLH
YPVLMRKICWLIVAAAWLGGSIDGFLTPVTMQFPFCASREINHFFCEVPALLKLSCTDTSAY
ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
YVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTTT (SEQ
ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTTCAGCAACG
CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGACCTCCATAGCCAGC
AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTCTT
25 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTCCACCATTTGTGCCAAAATGCTG
GTCCAGCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCAACACTTCC
TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC
GTAGCCATCTGCAACCCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCGTCACCAT
GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
GATGCTCCTCATCCCTTCTCTGTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
TGGTTGTCAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
GGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLGNGVIFGIICLDSKLHTPMYFFLSHL
40 AIIDMSYASNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHFP
QYTVIMSWRVCTILASTCWISFLMALVHITHLRPPFCGPQKINHFIQIMSVFKLACAGPRLNQ
VVLVYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM
YMAPKSRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
GCACTGGCGATTCTCCTCTGTGGACTCTTCTCTGTCTTCTATACACTCACCCCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC
TCTCACACCTGGCCATCATTGACATGTCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
TATTTGGCTTTTGCTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
GGCCATCTGCCACCCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG
GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
GCCGCTTTTGTGGCCACAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA
55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCCTATATGCGGGTTCTGCGTTCAT
CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTTGACATCCTGTGCGGCCATCTT

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTGTTGGGAATCTTCAGCCAGA
 TCTCACACCCTGGCCGCCTCTGCTTGCTTATCTTCAGTATATTTTGATGGCTGTGTCTTGG
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
 TATAAACCAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
 5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCTTGGGTGTGGCACCAGATGTAC
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTACAGCACTTCTTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCACTTTCAGTGTCTTACTACTATATCATCTCACCATCC
 ATAAGATGAACCTCAGTTGAGGGTCGGAAAAAGGCCTTACCACCTGCTCCTCCACATTAC
 AGTGGTCAGCCTCTTCTATGGAGTGCTATTTACAACATCATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTGAATCC
 15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFSSGGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTGNALL
 20 ILLIHSEPRLHTPMYFFISQLALMDLMLYLCVTPKMLVVGQVTGDDTISPSGCGIQMFFHLTLAG
 AEVFLLAAMAYDRYAAVCRPLHYPLLMNQVRVCQLLVSACWVLGMVDGLLLTPITMSFFFCQS
 RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLIHRMNSAAGRRKA
 LATCSSHMIIVLLLFASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCAGGGACTCTTTGCTGAGAGCAAGCA
 TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTCTTGATGGCCCTCACTGGGAATGCCC
 TCCTCATCCTCCTCATCCACTCAGAGCCCCGCTCCACACCCCATGTACTTCTTCATCAGC
 30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCCAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATACCATTTCCCGTCAAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCCTGGCTGGAGCTGAGGTTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
 GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCTTACCATGAGCTT
 35 CCCCCTTTGCCAGTCTAGGAAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCATCATGGTCATCTCCAGCTCATAACCCCTCATCCTGCATCTCATCCACAGGAT
 GAATTCTGCCGCCGCCGCGCAGGAAGGCCTTGCCACCTGCTCCTCCACATGATCATAGTG
 CTGCTGCTCTTCGGTGCTTCTTCTACACCTACATGCTCCGGAGTTCTTACCACACAGCTGA
 40 GCAGGACATGATGGTGTCTGCCTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 MDTLFICTTVPKLLADMVSKEKHSFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNVPHYCGSRNHHFCEIPAVILKACADTSLEYET
 LMYICCVLMLLIPISHSTSYSLILLTIHRMPSAEGRKKAFITCSSHLTVVSIFYGAAFYTYVLPQS
 50 FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACCSSAQKVATSDA (SEQ ID NO:
 477).

55 ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAAATTTGGT
 CATGATATTCTTGATTCAGGTGGACTCTCGCTCCACACCCCATGTACTTTCTGCTCAGTC
 AGCTGTCCATCATGGACACCCTTTTATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
 GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
STVMRPQVCALMLALCWVLTNIVALHTHFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE
5 MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVGKAFSTCSSHLVCVVCVFYGTLFSAYL
PPSIASEEKDIAAAAMYTIVTPMLNPFYSLRNKDMKGALKRLFSHRSIVSS (SEQ ID NO: 469).

ATGGAACCAATCCAGCATTTCTGAATTTTCTCCTCCGAGGAATATCAGCGCCTCCAGAGC
AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
10 CTCATCATCCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
CAACCTGTCTTTTGTGACATGGGTTTAAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGAAATGTATTTCTTTCT
GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
15 ATTGTGCTGGGTCCCTACCAATATCGTTGCCCTGACTCACACGTTCCCTCATGGCTCGGTTGT
CCTTCTGTGTGACTGGGGAAATTGCTCACTTTTTCTGTGACATCACTCCTGTCTGAAGCTG
TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTGTCTTGGGAGGCACCGTACTCA
TCGTCCCCTTTTATGCATTGTCACTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT
20 GTGTGTTCTATGGGACCCTCTTCAGTGCCTACCTGTGTCTCCTCCCTCCATGCTCTGAAGAG
AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPALAILLGLFSAFYTLTLLGNVIFGIIICLDCKLHTPMYFFLSHLA
IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVMSYDRYADICHPLRY
NILMSWRVCTVLAVASWVFSLLALVPLVLILRLPFCGPHEINHFEILSVLKLACADTWNQV
VIFAACVFILVGPLCLVLVSYLRLAAILRIQSGEGRRKAFSTCSSHLVCVGLFFGSAIVTYMAPK
30 SRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCCTTCTATACTCACCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG
AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
ATTTGGCTTTTGTCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCTATGATCGCTATGCG
GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGACTGTCTCTGG
CTGTGGCTTCTGCGGTGTTTCACTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCCTGAGG
40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
GGCCTGTGCTGACACCTGGCTCAACAGGTGGTTCATCTTTGCAGCCTGCGTGTTTCATCCTG
GTGGGGCCACTCTGCCTGGTGTGCTGCTTCTCCTACTTGCGCATCCTGGCCGCCATCTTGAGGA
TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT
GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLLLIHIDSSLHTPMYFFINQLSL
IDLTYSVTVPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR
YSVLMASHRVCLLLASGCWFVGSVDGFMLTPIAMSFPCRSHQHFCEVPAVLKLSGSDTSLY
KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNYML
55 PSSYQTPEKDMSSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPICALPTGGLLPHQPHTMMEIANVSSPEVFVLLGFSTRPSLETVLFIIVLSFYMVLSILNGNI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLG
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTTSMTVGSTLTMLLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFFVPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQGKFIALFYTVVTPALNPLIYTLRNTTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCTCCTGGGCTTCTCCACACGA
15 CCCTCACTAGAAACTGTCCTCTTCATAGTTGTCTTGAGTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCTTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCCAACCTCCCTTCCTGGACATGAGCTTCACCACGAGCATTGTCCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCTATGACCGCT
20 ACGTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
25 TGTCTTTGTTGTCTGCTGCTCTGGGGCTCATCCTGGTCTCTTACGGCCACATTGCCCGGGCCG
TGTTGAAGATCAGGTCAGCAGAAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCTTATTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

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AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIIVLLIYVTSIGNIMILLIKTDSRLQDTPMYFFPQHLAFVDICYTSAITPKMLQSFTEEN
NLITFRGCVIQFLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQT VYIQLVAGSYIIGSI
35 NASVHTGFTFSLSFCKSNKINHFFCDGLPILALSCSNIDNIILDVVFVGFDFLMFTLVIIFSYIYIM
VTILKMSSTAGRKKSFSSTCASHLTA VTFIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCCTTCTCTTGGTCTTTCTAGACTTTTGGTAGTCAT
GGGTGCGAGGAAACAGCACTGAAGTGACTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTGAGCATGTCCTTTTCATTGTACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTCAAACACCCATGTACTTTTTTC
CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGCGGGCTGTGTGATACAATTCTTAGTTT
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTACATTTTCA
CTGTCTTCTGCAAGTCTAATAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATTTCTGC
50 CCTTTTCATGCTCCAACATTGACATCAACATCACTATCTAGATGTTGTCTTTGTGGGATTGTG
TGATGTTCACTGAGTTGGTCATCATCTTTTCTCCTACATCTACATTATGGTCACCATCCTGAAG
ATGTCTTCTACTGCTGGGAGGAAAAAATCCTTCTCCACATGTGCCTCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAAATGAAAGTAGCCTCTATATTTTATGGCACTGTTATTCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAAATAA (SEQ ID NO: 468).

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTTCATGGATAATTGGTTTTTACACTCCATAAGCCAGATAGTTTAAACAAT
 GAACTTGCCTTTCTGTGGCCACAATGTCATAAAACAACATATTTTGTGATCTTCCCTTGTGA
 TCAAGCTTGCTTGCAATTGAAACATACACCCTGGAATTATTTGTCATTGCTGACAGCGGGCT
 5 GCTCTCTTTACCTGTTTCATCCTCTTGCTTGTTCCTTACATTGTCATCCTGGTCAGTGTACC
 AAAAAAATCATCATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG
 GTCACCTCTGTTCTTTGGACCTTGATTTTTATCTATGTTTGGCCATTGAGTGTGGCAAG
 CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 10 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTCCAATATGTTAGTT
 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQA VFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
 LALTDISFSSVTPKMLMDMRTKYKSILYEECISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRLSFCAANTIPHVFCDLAALLKLSCSIDIFLNE
 LVMFTVGVVVITLPMCLVSYGYIGATILRVPSTKGIHKALSTCGSHLSVVSLLYGSIFGQYLF
 PTVSSSIDKDVIVALMYTVVTPMLNPFYSLRNRDMKEALGKLSRATFFSW (SEQ ID NO:
 461).

ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTCACCCTGTTCTGCGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTCACACCCCCATGTAATTCT
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 20 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
 TTTTATAATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
 25 GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT
 AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCCTTCTCCTGACCC
 GGCTGTCTTCTGTGCTGCGAACACCATCCCCATGTCTTCTGTGACCTTGTGCGCCTGCTC
 AAGCTGTCTGCTCAGATATCTTCCCTCAATGAGCTGGTCAATGTTACAGTAGGGGTGGTGG
 30 TCATTACCCTGCCATTCTATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCTCTCTCTG
 TGGTGTCTCTTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTACACCCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
 35 CAACATTTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRPELQIPLFGVFLVIYELITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIHSEFFILSAMAYDRYVAICNPLL
 40 YYVIMSQRQLCHVLVGIQYLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
 LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGRKKAFTSTCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTCACAAGGCGGC
 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACTATGATCATTTTGACCAAACCTGGACTCCCACTTACATACACCTATGTACTTTTC
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCAATTTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCTATTATGCATGTGCTGCACAGCTGGCATTCT
 45 TTCTTATGTTTATTATCAGTGAATTTTTCATCCTGTGAGCCATGGCCTATGACCGCTATGT
 50 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG
 TGGCATTCAATATCTCTACAGCACATTTTCAGGCTCTGATGTTCACTATTAAGATTTTACA
 TTGACCTTCTGTGGCTCTAATGTCAATAGAAATGAGTGTGAGCATACTATTTTCTGTATTTAATT
 TATGCTTTGCTCAAATGCACAGGAAATAGAAATGAGTGTGAGCATACTATTTTCTGTATTTAATT
 TGATCTCCTCCTTTCTGATAGTCTTAGTGTCTTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCAATCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCCATTTGACAGTGG
 TGGTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCAATTGTACCCAAGATGCTGG
TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
TTCTCTTCTTTGGCTCCTCTCACTCCTTCCTGCTGGCAGCCATGGGCTATGATCGCTATAT
5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA
TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCCTGTCTTA
AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
CTTGGTCATTCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
10 AAATCCCTTCTCCTCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
GTAACCTGTTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
AAGCCAAGACACCCTAATATCTGTGTACATACCATCCTTACCCCATTTGTTCAATCCAATG
ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

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AOLFR244 sequences:

MWQEYYFLNVFFPLLKVCCLTINSHVVILLPWEYHLIWKILPYIGTTVGSMEEYNTSSTDFTF
MGLFNRKETSGLIFAIISIIFFALMANGVMIFLIQTDRLRHTPMYFLLSHLSLIDMMYISTIVPKM
LVNYLLDQRTISFVGCTAQHFLYLTIVGAEFFLLGLMAYDRYVAICNPLRYPVMSRRVCWMI
20 IAGSVWFGGSLDGFLLTPITMSFPFCNSREINHFFCEAPVLKLACADTALYETVMYVCCVLMMLL
IPFSVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSFLFYGAAMYTYMLPHSYHKPAQ
DKVLSVFYITLTPMLNPLIYSLRNKDVGTGALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTGGCCATCATCTCT
ATCATCTTCTTACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTCTTAATTGACATGATGTAT
30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTG
CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCTCTGAGATACCCTGTCC
TCATGAGCCGCGGGTCTGTTGGATGATTATAGCAGGTTCTGGTTTGGGGGCTCTTTGGA
TGGCTTCTCTCTAACCCCATCACCATGAGCTTTCCCTTCTGCAATTCCCGGGAGATTAACC
35 ACTTCTTCTGTGAGGCACCAGCAGTCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTCTCTGTAGTCCTTGCTT
CCTATGCCGAATCCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG
CATTTGCCACTTGCTCATCCACATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC
ACCTACATGCTGCCACATTCTTACCACAAGCCAGGCCAGGACAAAGTCCTCTCTGTGTTTT
40 ACACCATCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT
CTTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

MDLKNGLVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPYFLLGN
45 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIIMAFDRYVAICKP
LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMLNLPFCGHNVINIFCDLPLVIKLACIETYTLE
LFVIADSGLLSFTCFILLVSYIVILVSVPKKSSHGLSKALSTLSAHIIVTLFFGPCIFIYVWPFSSL
ASNKTLAVFYTVITPLLNPSTYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

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ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
GGGAACTTCAAATTTTCTTCTTGTGACATTTCCCTGATCTACGGTGCTACTGTGATGGGA
AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCTTCATTCTCCCTGTACTTTCT
CCTTGGAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA
55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFIYLRPTANYVSNKDRLVTVTYITIVTPLLNPVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGGCAA
TGTCACCATTATCAGTGTACATCCACCTGGATAAAAAGCCTCCACACACCAATGTACTTCTTCC
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCAATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTTATGATCGCTATGCTG
CCATTTGTCAACCTCTGCATTACCCCACTTATGAGCTGGCAGGTGTGTGGAAAACTGGC
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTTACAGTAGTAAATTTAGTTTTAGCC
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACAATTTGTGATATTCAATTTGTGGAGTTCTTGTAT
TTGTGGTTCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCTGGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTTG
TTATTGTTTATTATGGCTGTGCTTCTTCTATCTACCTGAGGCCTACAGCAAACTATGTGTCC
20 ACAAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAATTGCTATCAGAAAAGTGTTGGGCAAGAAA
GGTTCTCTAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLLGIPGLESMHLWVGPFPAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIPLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGIA RLSCASIRVNIY
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFTSCGSHVCVMLTFYMPAFFSFMTHFRGR
NIPHFHILLANFYVIPPALNSVIYGVRTKQIRAQVLKMFFNK (SEQ ID NO: 453).

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ATGAATACCACTCTATTTTCATCCTTACTCTTTCCTTCTTCTGCGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTTCTTGTCTGTGTTCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTTGTGATTCAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTCTG
GCCATTCTGTATCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTTCATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCTCTTTGCTACACGTTGGTGTGACAAACAAGGTGGTGTGAGTTATGGCA
CTGGCCATCTTTCTGAGACCTTAGTCTTTGTCTATACCTTTGTTCTATTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC
40 CTGTCTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCAATTTCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTGACACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTCTCATTGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAGTGCTGAAAATGTTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNTVVRVREFVVLGFSSRLRLQQLFVIFLLLYLFTLGTNAIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLSQHSFG
SQLVIFMLGVFALVIPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFIYLRPK
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRRTIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

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AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQAIFFLHFTGGAEMVLLVSMAYDRYVAIC
KPLHYMTLMSWQTCIRLVLASWVVGFBVHSISQVAFVNLPCGPNEVDSFFCDLPLVIKLACM
10 DTYVLGHIMISDSGLLSLSCFLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV
YVRPFSRFSVDKLLSVFYTIFTPLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

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ATGGACCCACAGAACTATTCTTGGTGTCAGAATTTGTGTTGCATGGACTCTGCACTTCAC
GACATCTTCAAAATTTTTCTTTATATTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
CCTGTGGGGAACCTAGCTTTCTGGACATGTGGCTGGCCTCATTGCCACTCCCAAGATG
ATCAGGGATTTCCTTAGTGATCAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
TCTTCTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAACCCTTGCAATACATGACTTTGATGAGTTGGCAGACTTGCATC
AGGCTGGTGCTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA
CTGTAAATTTGCCCTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
GTGATCAAACCTTGCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
GGTTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTGTATGTGCGGCCTTTAGTAGGTTT
TCTGTGGACAAGCTGCTGTCTGTTTTATACCATTTTTACTCCACTCCTGAACCCCATAT
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAACCGACGGGT
GACTTTTCAATGA (SEQ ID NO: 448).

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AOLFR240 sequences:

MAGENHTTLPEFLLGFSDLKALQGFLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAAQMYVFIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR
SEISVMTATIVFIMIPFSLIVTSYRILGAILAMASTQSRKVFSTCSSHLLVVSLLFFGTASITYIRPQ
35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNKDVRRLRHLVKRQRPSP (SEQ ID NO: 449).

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ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG
TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCATGTACTTCT
TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCT
GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
TACGTCTTCATTGTCTGCGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
GATATGTTGCCATCTGCCAGCCCCTACGCTATTCACCCCTCTTGAGCCCACGGGCCTGCTT
GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCCATGCCTCCCTC
ATCTTCTCTCTACCTTTTCGACGCCACCCGATCATCCCGCACTTCTCTGTGACATCCTGCC
AGTACTGAGGCTGGCAAGTGCTGGGAAGCAGGAGCGAGATCTCCGTGATGACAGCCAC
CATAGTCTTCATTATGATCCCTTCTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG
CCATCCTAGCAATGGCCTCCACCCAGAGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
TCTGCTCGTGGTCTCTCTCTTTGGAACAGCCAGCATCACCTACATCCGGCCGACAGGCA
GGCTCCTCTGTTACCACAGACCGCTCCTCAGTCTCTTCTACACAGTCATCACCCCATGCT
CAACCCATCATCTACACCCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAGCGCCCCCTACCCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

55

MPQILIFTYLNMFYFFPPLQILAENLTMVTEFLLGFSSSLGEIQLALFVVFLFLYLVLSGNVTHIS
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLNLLSVARTISFNCCALQMFFFLGFAITNCLL

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
 GTGGGCCTTGCCACATTGCCTACTTCTTCTGCGACATAACCCCTGTCTAAAGCTCGCCTGT
 ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCCAGGGCCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA
 10 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFTFLELVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
 RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRYIAISKPL
 15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCNPNVLDTFYCDVPQVLKLACTDTFT
 LELLMISNNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIYVYA
 RPFTALPTDTAISVTFTVISPLLNIHYTLRNQEMKLAMRKLKRRLLGQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
 AAACCTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCCCTCCATCACAGCTCCTAAGGTCCTG
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGTGATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCCTGGGTGGGGGGCTTGTCCTACTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC
 TCAAACCTTGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGTCTCACACTGGGGAAGGCAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG
 TGGTGACCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCCGCCCTTCACTGCCCTCCCC
 ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCTTTGCTCAATCCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTVSSPELQIPLFLVFLVLYVLTMAGNLGIITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 40 LLYMVVSRRLCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCYDIAPLLALSCSDTYIPE
 TIVFISAATNLFSSMITVLVSFNVLSILRIRSPEGRKKAFTSCASHMIAVTVFYGTMLFMYLQP
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTTACACAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACAGTGTTGACTCTCGACTTCAAACCCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCAATTGCCCTAAAATGCTG
 ATGAACTTTTATGTAAGAAGAAAACCTCACTTCTATGAATGTGCCACCCAACTGGGAG
 50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC
 TCTGTGTCTTATTGCTCTTCTAATAATAATCAATCATTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGCTCTGATACTTACATACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTGTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA
 AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTGCGGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 10 GCGGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTGCTCGGGTT
 TCCAAGAGGAGCAGACAGAAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCCTATTATTTA
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTIILLRLEARLHTPMYFFLSNL
 SSLLDAFATSSVPQMLINLWGPCKTISYGGCITFLYVFLWLGATECILLVVMFAFDYVAVCRPL
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY
 LLPAKNSKQDQGFISLFSYLVTPMVNPLIYTLRNMEVKGALRRLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTGCTACTAGTTCAGTCCCCCAAATGCTGA
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCTTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACCTCT
 GCAGCTCCCATTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
 GATCAAACCTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGCGTTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGACACAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA
 ATCCCCTCATCTACAGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSTVTVPKVMAGLLTLDGKVIS
 FEGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
 45 AAHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLLIVISYIFIVA
 AVLRIRTAQGRQRAFSPCTAQLTGVLVYVPPVCYIYQPRSEAGAGAPAVFYTIVTPMLNPFYI
 TLRNKEVKHALQRLLCSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAAATGTCAGTTTTGTTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGGGTACACCGCTAAACATTCTAGCCTCTT
 CTTCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTGGGGCACCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDMMVSVFYTILTPVVNP
LIYSLRNKDVGMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA
CTGTGACGCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA
10 GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTCTCTTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCTCATGAACCATAGGGTGTGTCTTCTCTGTCATCAGGCTGCTGGTTCCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCTTCCGTGGATCCCGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCTCCTCATGCTCCTCATCCCTGTGGTGATCAT
TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACACTCAGCAGAGGGCCGGA
AAAAGGCCCTTGGCACCTGCTCCTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFILMGLFRRSKHPALLSVVIFVFLKALSGNAVILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI
LSCSDTSLYETLMYLCCVLMMLIPVTIISSSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDMMVSVFYTILTPVLNPLIYSLRNKDVGMGALKKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACACTGTGACGCCACCTCCACAGCC
CCATGTACTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCCGAATTTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCTCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCCTCATGTACCTA
TGCTGTGCTCATGCTCCTCATCCCTGTGACGATCATTTCAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGA AAAAGGCCTTTGCCACCTGCTC
CTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCCCTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATTCTGCTCTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTISKAGCVAQVFLVFFVYVELLFLTIMAHDRYVAVCQPL
HYPVIVNSRIQIMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCTDTSNE
VMIVVSALGVGGGCFIFIIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVSVFLSSCSSVYLRPP
AIPAATQDLILSGFYSIMPPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTATGTTGTATTGGTAACTCTAATGGGAAACATC

AOLFR230 sequences:

MGMEGLLNQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMD SRLHTPMYFLLS
QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTIGGEFFLLGLMAYDRYVAVCNP
LRYPLLMNRRVCFLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSCDTDS
5 LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSEAEGRRKAFATCSSHIMVVSIFYGAAFY
TNVLPHSYHTPEKDKVVSIFYTILTPMLNPLIYSLRNKDVAALRKVLGRCGSSQSIRVATVIR
KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
10 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
GCCAACTTGGTGATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
CTTGCTCAGCCAGCTCTCCATCATGGATAACCATCTACATCTGTATCACTGTCCCCAAGATGC
TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCCTGGGCTGTGCAGTTCAGATCTT
CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCCTGCTGGGTCTCATGGCCTATGACCGC
15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
CATGGTGGTCGGCTCCTGGGTTGGTGGTTCCTTGGATGGGTTTCATGCTGACTCCTGTCACT
ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT
GCTGAAGTTGTCTTGCACAGACACGTCACTCTATGAGACCCTGATGTATGCCTGCTGCGTG
CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCCTACACGCACATCCTCCTGACTGT
20 CCACAGGATGAACCTGCTGAGGGCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
ACACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCCCATGCTCAA
CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
GAGATGTGGTTCCTCCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
25 NO: 430).

AOLFR231 sequences:

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFDSSLHTPMYFLLSNL
SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMAIDRYVAICKP
30 LHYMTIMSPRVLTGLLLSSYAVGFVHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI
LQLLVIADSGLLSLVCFLLLVSYGVIIIFSRYRAASRSSKAFSTLSAHITVVTLLFAPCVFIYVW
PFSRYSVDKILSVFYTIFTPLLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

ATGGAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
AACCTGCTCATCTTGGTGACTGTGACCTTTGATTGCTCCTTCACACACCAATGTATTTCT
GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGTACCCCTAAGATGATTG
TAGATTTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATCCCAGATGTTCTT
TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCCACGGGTGCTCACTGGGC
TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTCATGTTG
ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCCCTTGTGAT
TAAACTTGCCCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
CTGTCACTGGTCTGCTTCCCTCCTTCTTGGTGTCTCCTATGGAGTCATAATATTCTCAGTTAG
45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG
TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
GATAAAATTCTTTCTGTGTTTTACACAATTTTACACCTCTCTAAATCCTATTATTTATAC
ATTAAGAAATCAAGAGGTAAGAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:
432).

50

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
VIFVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTPKMLLDQVMGVNKKIS
APECGMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLS CSDTSLYEIFMYLCCVLMLLPVVVISSSYLLILL

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCAATTGTA
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTHIGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFMLHRGLCARLVVSWCTGVSTGFLHSMMSRLDFCGRNQINHFFCDLPPLMLQLSCSRV
10 YITEVTIFILSIAVLCICFFLTLPYVFISSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMMISMVY
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC
15 TTGAATGGCAGGCCCTGCTCTTTGTCAATTTTCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTCATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCCTTCTCCTA
GCCAACCTGCTGTCTGGGGCCAAGCCATCTCCTTCTCTGCCTGCATGGCACAGCTCTACT
TCTTCGTATTCCTCGGCGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACCGTTAC
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTGACACAGGCTTTCTGCATTCCATGATGATTTCC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTCTCCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCAACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTGATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIVAAAWLGGSIDGFLLPVTMQPFCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVTGALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTTATCATATCTCTTTTCGTGTACCCTACAGA
40 GCTATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTTGTGCCCAAAATGCT
GGTGCAGCCAGGTGATGAGCCAGAGGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCA
TGCAGTTCCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGTCTGTATTA
50 TGATGCTCCTCATCCCTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCACTCATTTACAGCCTTAGGAACAAGGATGTCACGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

GCTGCTGTCTGTCTGCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCT
 GGCTATCGCCTCCTGGGGTGC GG GTTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCCGAGTCATAGT
 5 CGTGGCTGTTCTGTCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
 GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTCTCAATCCTC
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQSTDFILLGLFPFSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLIRM
 15 SKRVCVLMITGSWIIGSINACAHTVYVLIHIPYCRSRAINHHFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA
 20 TAATTGACCTTTTCTTCTTCATTCTCATTGTTTTCATTTCCTGATGGCTCTAATTGGAAACC
 TGTCCATGATTCTTCTCATCTTCTTGACACCCATCTCCACACACCCATGTATTTCCTACTG
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATGTTTCTTAAGATGGCATCTGA
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTGAGAGTTTCTTCTCT
 TGGCATTAGGAGGTGCAGAAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
 25 TATTTGCTTTCCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTGTAGTGCCACCATCTTTC
 TCGTGTTCCTTTCATTGGTATTTTCATGTTTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
 30 ATGAAATCTGCAGAAAGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
 GTAACCTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIWYVTVTIPKMLAGFVGSQDHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
 40 NLSCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVCVHIF
 YAASIFTYARPKALSAFDTNKLVSPLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHDPDP
 KKASRVN (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
 45 CCTGCGCCACTACAGGTACTATTGTTTGGCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCCATGTAC
 TTTTTCTAGCTAATATGTCCTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
 ATGACACAGCTCTACTTTTTCCTTGGCTTGGGCTGCAGTGAGTGTGTCTCTCGCTGTTAT
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTGAGTGGCC
 GGCTGTGTGTGCAGATGGCTGTGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
 ATGCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTT
 ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
 55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCTATGCTCGGCC

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTTGCCCTTGTTCCCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 CCTTTCCCTTCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCCAGATGTTCTT
 TTCTGCCTCATGGGCCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCCAGCT
 GGTCACTACTTCTTCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCTCTGCTGAGGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTATTATGGCTGTGCTTCTTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 HLSFADLCFASVTPKMLANLLAHDHSISLAGCLTQMYFFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMWL VSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLRLSC
 SDTHHIQLLIFTEGA AVVVT PFLILASYGAIAAAVLQLPSASGRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSRREA EWGRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTTCGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGTCTTGTATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCACCTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCCAAGATG
 30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCACGTCCTCCCTCCTGTATATCCTTCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCCACCAAGTGCCCCACTTCTTCTGTGACCACCAAGCCT
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTCACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCCTCGCCTCCTATGGGGCCATCGCAGCTGC
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTCATGTACACTGTAGTCACCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTIIIALSWLDLRLHTPMYFFLSHLSL
 45 LDLCFTTSTVPQLLINLCGVDRITITRGGCVAQLFIYALGSTEVCVLLVVMADFDRYA AVCRPLHY
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRAFGTCGSHLLVVFLFYGSAIYT
 YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCAACCACAGCACCGTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATCACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTTGACCGCTAT

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIHVILGMHSAEGHHKAFST
CAAH LAVFLFFGSVAVMYLRF SATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQK RAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCCTTTATTCCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTTCATTGTCATCCAGGTGGGCATGGC
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCCTGGGC
TGGCTGCCTCCTGCAGATGTACTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCCTCCTTGCT
CTTCCTGAGATTGCATGGATTTCCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGCCCTGCACAGATACATTCCCTAGTGCTCATT
GTGGATGCCATCCATGCAGCGGAAATGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCATGTATT
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTATC
20 CTGCTCCCTTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPPTPPLQLLLFVLFFAIYLLTLENALIVFTIWLAPSLHRPMPYFFLGH
LSFLELWYNVTIPRLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGS GFSSMMKLLFISQLSYCGPNIIHFFCDISPLNLTCS DKEQA
ELVD FLLALVMILLPLLA VSSYTAIIAILRIPTSRGRHKAFSTCAAH LAVVVIYSS TLFTYAR
PRAMYTFNHNKIISVLYTIIVPFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTC
35 CTTGGCCATCTCTCTTTCCCTGGAGCTATGGTACATCAATGTCACCATTCCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTATTTCCTCAA
40 TTGTCCTACTGTGGACCCCAACATTATCAACCACTTTTTCTGTGATATTTCCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTTCAAGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIHAIRLDSHLHTPMYFLSLFL
SFSETCYTLGIIPRMLSGLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVITSFLTGYLFG LGM TLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLVLLVSFFFITISYAYILAILRIPSAEGQK KAFSTCASHLTVVIIIHYGCASFVYLRPK
ASYS LERDQLIAMTYTVVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

AOLFR218 sequences:

5 METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA
 LLDIWYSSITAPKMLIDFFVERKIIISFGGCIQFLFLHFVGASEMFLIVMAYDRYAAICRPLHYA
 TIMNRRLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLVMFGPSIYIYARFPD
 SFSLDKVVSVFHTVIFPLNPIIYTLRNKEVKAAMRKVVTKYLCEEK (SEQ ID NO: 407)

10 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 GGGAGGTCCAACCTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 AATATCCTTATCATTTGCACCATCAGGCTAGACCTCATCTGACTTCTCCTATGTATTTCTCCT
 GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTCCATTACAGCCCCCTAAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
 15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCTATATAATACAGGTGGCTCTCATTGTT
 CGACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTG
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
 GATCTCTGTGGTGTGTTTCTGCTGTGTTAAATGTCCTATGCCTTCCTTCTGGCCTTGCTCA
 20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACAT
 TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCTACTGTAATATTCCCTTTACTTAATCCCATT
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
 ATTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

25

AOLFR219 sequences:

MLTSLTDLCSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLLTFSLLYLAILLGNF
 LIILTVTSDSRLHPTMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
 30 EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLSPFCGN
 KVDSFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVSYSYTVILVTVNRNSSAMAKAR
 STLTAHITVVTLLFGPCIFIYVWPFSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS
 RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

35 ATGCTCACTTCATTAAGTATCTCTGTTTCTCTCCTATTACAGGTAGCTGAAATTAAGTCCCT
 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
 TCTAGTTCAAGGGAGCTCCAACCTTTCTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
 TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
 TGTACTTTCTGCTTGCAAACCTGTCAATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
 AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
 40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
 GTGTTGTGCTCGTCTCATTTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
 TTCACTGTTAATCTGCCATTTTGTGGTCTTAATAAGGTAGACAGTTTCTGTGACCTTCC
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTGACGTTACTAATAGTTGCAGAT
 45 AGTGGCTTTCTTTCTCTGAGTTCTTTCTCCTCTTGTTGTCTCCTACACTGTAATACTTGT
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
 TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
 TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTACGCTTATTTTAAACCCTGT
 AATCTACACGCTAAGAAACAAGAAGTGAAGGCAGCTATGTCAAAACTGAAGAGTCGGTA
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
 (SEQ ID NO: 410).

AOLFR220 sequences:

55 MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGLLFFIPLLLIYG
 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
 HSLGITESCVLTAIDAIDRYIAICNPLRYPTIMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGGTGTCCG
 ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTGGCCACATCACAGTG
 GTCATTCTTTCTTCGGGCTTGCATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTTGAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT
 CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL
 10 TNLSDMSLASFATPKMITDYLTHGKTISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPL
 HYASVISPVQVCVALVVASWIMGVMHMSMSQVIFALTLPCGPYEVDSEFFCDLPVVFQLACVDY
 VLGLFMISTSGIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
 PLSSFLTDKILSVFYTIPTLNPIIYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACTACAGATGTTTTCTTTATGGTGTTCATTGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTCGCCACCCCAAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAAGTGAAGTATCTTACTCATGGCCATGTCCTTTGATAGGTAT
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTGATTAGTCCCAGGTGTGTGTTGCTCT
 CGTGGTGGCTTCTCGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
 ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCTGTGGTGTT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGCTGTTTATTGTTTTATTAAATTCATATGTTATTGTCTGGTTACTGTGAA
 GCATCATCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTCAATTGTTG
 TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTCTCACA
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 35 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISEFGCMTQMFFLHLLGGAEIVLLISMSFD
 RYVAICKPLHYLTIMSRMCVGLVILSWIVGIFHALSQLAFTVNLPFCGPNEVDSEFFCDLPVVIK
 LACVDYIILGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGSSKALSTCSAHFTVVTLPFFGP
 CTFIYVWPFTNFPIDKVLVSVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCTGTTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTCATCA
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGTGAGATTG
 TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGGATTGTGCGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTCGACACATATATTC
 50 TGGGGGTGTTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTGGT
 GATCTCTTAACTATCATCCTGGTCACCGTTCCGGCAGCGTCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCTTTTCTTTGGCCCATGCACTTT
 CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACTCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTGGCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCCTCTCTGTGGCAACCATAGGCTGGACCAATTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTTGTTGTTAGTGTTCTGT
 TTGTTGTCAATCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIHLTVTSDTSLHSPMYFLLGN
 LSFVDICQASFAATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVIMSRRTCTVLVMISWAVSLVHTLSQLSFTVNLPFCGPNVVDSEFCDLPRVTKLACLDSEYIE
 ILIVVNSGILSLSTFSLLVSSYIHLVTWVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 20 PLDKFLAIFYTVFTPLNPIIYTLNRNRMKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAAAGTCCAGCTTTTCTATTTTGTCTTCTCTGTGTTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
 25 CTTGGGAAACCTTTTCTTTGTTGACATTTGTCAGGCTTCTTTTGCTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGCACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTTACTGTG
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAACTTGCCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAAAT
 CTTTCCCTAAGCACTTTCTCTCTTGGTCACTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTCACTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATATTATTCTTTGGACCTTGCATCTTCTATGTGTGGCCCTTTACCATCTCTCCTTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTACCCCCGTCCTAAACCCCATATTATTA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGLHSVSHLAFTVDLPFCGPNEVDSEFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALISYTHILIGVRCRSSGSSKALSTLTAHITVVILFFGPCIFYIWPFSRL
 45 PVDKFLSVFYTVCTPLLNPIIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCAATTATTTCTTTTACTCCCATTTGAACTCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTTCAATTGATATCTGTCACTAATTTGCCACCCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCCAGATATTCGTT
 CTTACAGTTTTGTTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCCTGGGCGGTGGCGTTCTTCACTTCTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

5 ATGATGGGTAGAAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 10 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC
 TTAGCGAACTTACTGACTTCCAATAATTTCCCTTACGGGGCTGCTTTGCCAGATGTTCTT
 TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCCATGATCGCTATG
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 15 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTA
 GCTCTGTCTGCACTGATACATAACAACCCGAAATCCTGATATTCAATTATTGTTGGTTCCAC
 CCTGATGGTGTCCCTTTTCAACAATATCTGCATCCTATGTGTTCACTTCTTTTACCATCCTGA
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCCTCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCTT
 20 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT
 CATTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFIYLFVTLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSSVTVPKALVNFQSNRRSISFVGCFVQMYFFVGLVCCECFLLGSMAYNRYAICNPL
 LYSVVMQKVSNNWLGVMPIYVIGFTSSLISVWVISSLAFCDSINHHFCDTTALLALSCVDTFGT
 EMVSFVLGAGFTLLSSLLIITVTYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLPD
 25 NTSSLTQAQVASVFYITIVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAAATCACC
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCACTGTTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTT
 30 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTGGCTGCTTTGTTCAAATGTACTT
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTAGTAGTCATGTCCAAAAAGTGCCAAGTGGCT
 GGGAGTAATGCCATATGTGATAGGCTTACAAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTGTGACACCACAGCTCTTTTAGC
 35 ACTCTCCTGTGTAGATACATTCGGCAGCAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTAGCTCTCTCCTTATCATCAGCAGCACTTATATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGAGGAGGAGGCTTCTCCACCTGCGCATCCACCTCATGGCT
 GTAACATCTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCATTCCCATGCTGAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDHPR
 EAVLVFVFLFFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVIMNPRLCQQLASISWLSGLA
 SSLIHATFTLQPLCGNHRDLHFICEVPALLKLACVDTTVNELVLFVVSFLFVIPPALISISYGF
 50 TQAVLRIKSVEARHKAFSTCSSHLTVVIIFYGTIIYVYLQPSDSYAQDQGFISLFYTMVPTLNP
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCTAATGGATTTATCCTTCTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCTTTCTTCTACCTCCTGACCTTGTGGGA
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTCATACCCCAATGTACTTTT
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

AOLFR209 sequences:

- MDKINQTFVREFILLGLSGYPKLEIIFLILVMYVVILIGNGVLIHASILDSRLHMPMYFFLGNLS
 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLLGMMAFDRYVAICNPLRY
 5 PIIMNKVVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV
 TLAVSNAFLVLP LLVIFFSYMFILY TILRTNSATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)
- 10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
 CCAAACCTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
 AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
 CCTGGGCAACCTCTCTTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGAGATGTTCTT
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCCTTGGCATGATGGCATTGATCGTTAT
 GTGGCCATCTGTAAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
 TGACTTCTGTATCATGGCTTTCTGGTGGAATCAATTCAACTGTGCAAAACATCACTTGCCAT
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
 TAAATAGCTTGTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGCAAAATATTGCT
 20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTCTCTATATGTTTCATCCTCTACACCATCTTG
 CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
 TGGTGATCATATTTATGGTACCATCTTCTTATGTATGCAAAACCTAAGTCCAGGACCTC
 CTTGGGAAAGACAACCTTGCAAGCTACAGAGGGGCTTGTTCATGTTTATGGGGTTGTGA
 CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA
 25 ATATTTGCTGAGCAGGAAAGCTATTAACAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

- MMGRNDTNVADFILTGLSDSEEVQMALFMLFLLIYLITMLGNVGMILLIRLDLQLHTPMYFFL
 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMFCFVFLGTAECYLLSSMAYDRYAAICSP
 30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSMSRLHFCDSNIIHHFFCDTSPILALSCTDTDN
 TEMPLIFIIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTIMIFTYLPK
 RKSYSLGRDQVAPVFYITIVPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)
- 35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
 GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTCTTACTCACCTGTCAATTTATTGACCTCAGTTACTCAACTGTCGTACACCTAAAAC
 CTTAGCGAACTTACTGACTTCCAACATATTTCTTTCACGGGGCTGCTTTGCCAGATGTTCT
 40 GTTTTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
 GCAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGCCCAAAGGCTCTGCCTCGCTC
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT
 AGCTCTGCTCTGCACTGACACAGACAACACTGAAATGCTGATATTCAATATCGCTGGTTCC
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
 45 GAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG
 GGAGTCACCATCTTCTATGGAACATATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
 ACTCATTTATAGTCTTAGAAACAGAGAAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)
- 50 **AOLFR211 sequences:**
- MMGRNNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILLIRLDLQLHTPMYFFL
 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMFFFAFLGTAECYLLSSMAHRYAAICSP
 55 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSMSRLHFYDSNVIHHFFCDTSPILALSCTDTYNT
 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTYLPKPK
 SYSLGRDQVASVFYITIVPVLNPLIYSLRNKEVKNVIRVMQRRQDSR (SEQ ID NO: 393)

AAAGCAGTTGCTGTATTCTACACTATGATAA CTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIIFDLSHLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFI SFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIIFYGTIFFMYAKP
10 ESKASVDSGNEDIEALISLFYGVMT PMLNPLIYSLRNKDVKA AVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCTGCTGGTAGGGCTTTCTGCCCCACC
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGA
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGTATTTCTT
CCTCTGTAATCTTTCTTCCTCGACGTTTGCTACACAAGTTCTCTGTCCCCTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCCTTCTCTGGGTGTATGGTGCAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATAACCTGT CATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCAATAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTAGTATGACAGGGTCAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCTTCCACTGAAGGAAAAACATAAGGCCTTCTCCACCTGCTCAGCCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTC'VQIAAGSWMTGCLTAMVEMMSVLPLSLCGNSIINHFTCEILAILKLVCVDT S
LVQLIMLVISVLLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGTALSMH
35 LKPSAVDSQEIDKFMA LVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFN TAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTTCTTCCTGGGATTTTTTCACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAACCTTTGTTTCAGGGAGAAACACTATTTCAATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATAACCTGT CATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAAATGATGTCTGTGCT
GCCACTGTCTCTCTGTGGTAATAGCATCATCAATTTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGCTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCCACCTGA
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

CACATTTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
CCATCTGCAAACCTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCCTGGT
GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTGAGATTCTCTTTACAGTATGG
CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTAAAA
5 ACTTGTTTGCATAGACACTCATACCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
GCTTATTAAACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG
TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACCTGCCCCATTGAT
AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC
10 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAGTGACTTCAG
ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIILPGNFLIIFTIKSDPGLTAPLYFFLGNLAF
15 DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFHLFLGGGEGLLLVMAFDRIYAICRPLHYPT
VMNPRTCYAMMLALWLGFFVHSIIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
LMVFNSGLMTLLCFLGLLASVAVILCRIRGSSSEAKNKAMSTCITHIIVIFFMFGPGIFYTRPFRA
FPADKVVSLFHTVIFPLLPVITYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)

20 ATGGAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT
CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTAAATATTCTACTTCATCATCCTCCCTGG
AAATTTTCTCATTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCT
TTCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG
GTGGACTTCTCTCTGCGAAGAAGATAATCTCTACAGAGGCTGCATCACTCACTCTTTT
25 TCTTGCACTTCTTGGAGGAGGGGAGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA
CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTATGAACCTAGAACCTGCTATGCA
ATGATGTTGGCTCTGTGGCTTGGGGGTTTGTCCACTCCATTATCCAGGTGGTCTCATCCT
CCGCTTGCTTTTGTGGCCCAAACCAGCTGGACAACCTCTTCTGTGATGTCCACAGGTC
ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC
30 TGATGACACTCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA
CGAGGGTCTTCTTCTGAGGCAAAAAACAGGCCATGTCCACGTGCATCACCCATATCATTG
TTATATTCTTCATGTTTGGACCTGGCATCTTCACTACACGCGCCCTTACAGGGCTTTCCCA
GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCTTTGTTGAATCCTGTCAATTA
TACCCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC
35 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVVSIVYINAMIGNVLIVVTTTASPSLRSPMYFFLAYLSFI
DACYSSVNTPKLITDSLKENKTILFNGCMTQVFGEHFFRGVEVILLVMAYDHYVAICKPLHYT
40 TIMKQHVCSLLVGVSWSVGGFLHATIQLFICQLPFCGPNVIDHFMCDLYTLINLACTNHTLGLF
IAANSGFICLLNCLLLLVSVCVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCIFYVMRPPATL
PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIRKLCRKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
ATGCAGAAAATCATATTTGTTGTGTTTTCTGTCATCTACATCAACGCCATGATAGGAAATG
TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTTCTG
GCCTATCTCTCCTTTATTGATGCCTGCTATTCCTCTGTCAATACCCCTAAGCTGATCAGAGA
TTCATCTATGAAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA
CATTITTTTACAGAGGTGTTGAGGTCACTCTACTTACTGTAATGGCCTATGACCACTATGTGG
50 CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT
GGGAGTGTATGGGTAGGAGGCTTCTTCATGCAACCATAACAGATCCTCTTCATCTGTCAA
TTACCTTTCTGTGGTCTAATGTCATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA
TCTTGCCCTGCACTAATACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTCATAT
GCCTGTTAAACTGTCTCTTGTCTCCTGGTCTCCTGCGTGGTCATACTGTAATCCTTAAAGACC
55 CCAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTCTCCACATCACAGTTGTCA
TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

ETLNSDDLDATDKLIFIFYRVMTPMMNPLIYSLRNKDVKEAVKHLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATTCTGGTGGGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCTTTCTGGCTGTGCAGTGCAGATGTTCCCT
CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
10 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCTGCTGTGACCACAACAT
TGTTCTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC
15 TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACTTCTCATGTACATGAAGCCCAAGTCTCAAGA
CTGTGGTGATAACATTCTGTGGGACCATTCTCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTGAGTACTGGATGCCACTGACAACTTATATTATCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAACACCTACTGAGAAGAAAAAATTTTAAACAAGTAA (SEQ ID NO: 376)

20

AOLFR203 sequences:

MKRQNSQSCVVEFILLGFSNFPQLVQLFGVFLVITYVVTLMGNIAITVIISLNQSLHVPMYLFLN
LSVVEVSFSAVITPEMLVVLSTEKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVSFPFCGPNEINHLFCETPPVLELVCACTFLF
25 EIYFTGTILIVMVPFLLILLSYIRVILFAILKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKTLLKLWRRKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACCTACCCAGTGATTATGAACAGAGGGGTTTTTATGAAA
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTGATCCTCTTGCTTACATTGAGTTCTGTTTGCCATCCT
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCCTTTTCCACCTGTGCCTCTCACCTCACA
40 TCTGTGACCCTGTTCTATGGCAGACCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAAACTGATCTCATTTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

AOLFR204 sequences:

45 MEKKKNVTEFILIGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKKIISFNGCMAQAYAHEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAVVGGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLILVVSIVILRSLKNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRSVTTLPI
50 DKAVAVFYTMVVPMLNPVVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTTCTG
55 ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTTACGCTCCTAAGTTGATTGTGA
TTCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

AOLFR200 sequences:

5 MTRKNYTSLTEFVLLGLADTLELQIILFLFFLVYITLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDSNVIIHFFCDSPPLFKLSCSDTILKE
SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRRTSSFL (SEQ ID NO: 371)

10 ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGTGATTATACACTTACAGTACTGGGA
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCCATGTATTTCTT
CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACCTCACTACCATCACCCCAAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTTGTGCTGGCTGCTTCTACAGATGTACT
15 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTTAATGGCCTATGACAGGTA
TGCGGCCATATGTGCGCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
ATGGCAGCCGGGGCTTTTGTGCTGCAGGGTGTCTGAACCTTCATGGTCAACACAAGCCATGTCA
GCAGCTTGTCACTTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
TTCAAGCTCTCTTGTCTGTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
20 TGAATATTGTGGGGACTCTGCTTGTGATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
TTTTCTATGCATTGCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCAGCTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCAGCTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCAGTGTGAATC
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA
25 GGAAAAGGACCTCTTCTTTCTGTGA (SEQ ID NO: 372)

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSIPSTLVSLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDYVAICNPLR
30 YPIIMSKDAYVPMAGSWIIGAVNSAVQSVFVQLPFCRNININHTCEILAVMKLACADISDN
EFIMLVATTLFILPPLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDL DATDKIISM FYGVMTPMMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
373)

35 ATGGAATGGGAAAACACACCATTTCTGGTGAATTTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGACGTGCAGATGTTCTT
40 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATCTGGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTTATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTGTGAGCATC
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCTCTACCTGTTTACGCCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCTCATGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
50 GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSIPSTLVSLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDYVAICNPLR
55 YPIIMSKDAYVPMAGSWIIGAVNSAVQTVFVQLPFCRNININHTCEILAVMKLACADISGN
EFILLVTTTLFLLTPLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
AAGCTGGCTTGTGTGGGCACCACGTTTAAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT
TCCTTATAGTGCCTGTCTCATTATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTTG
AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTGCGGACCTGCTTCTCCACCTGACA
5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMA YDRYAAVCKP
LHYTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHS AKGHQKALSTCASHFTAVSVFYGT VIFITLQ
15 PSSSHSMDTDKMASVFIAMIIPMLNPVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
TACAGATCCCCCTCTTTATCTTGTTACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
GGGATGATGTTGCTGATCCTGATGGACTCTTGCTCCACACCCCCATGTACTTTTTCTCAG
20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTGATGTTCTTCTTTGT
AGCCTTGGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCTGTCTGGCCC
TAGGCTCATATGTCTGTGGCTTCTAAATGCCTCATTCCACATTGGGGGCATATTCACTCTC
25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
TTTTTGTTCTTCTAGTTATCTTTATCTCCTACTTGTTTCATATTCATCACCATCTTGAAGATGC
ATTCACTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGACGCCAGCTCCAGCCACTCCATGGAC
30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCCTGTGGTCT
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCCAAAAAT
TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

MDTGNKTL PQDFLLGFPGSQT LQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
35 NLSFLEIWYTAAVPKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLLAAMAYDRCLAICY P
LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA
VELVAFVIAVVVILSSCLITFVS YVYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
TSIKDALDLIKAVHVLNTV VTPVLNPFYITLRNKEVRETLKKWK GK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT
TCTGAGCAACCTCTCCTTCTGGAGATTTGGTATACCACAGCAGCAGTGCCCAAAGCACTG
45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTACAAGCTGTCTTTGACAGATGTACT
TTGTTTTCTCATTAGGCTGCACAGAGTACTTCTCCTGGCAGCCATGGCTTATGACCGCTGT
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
TGGCCCTGGGCTCCTGGGTGTGTGGTTTTCTGGCCATTGCAGTGCCACAGCCCTCATCAG
TGGCCTGTCTTCTGTGGCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
GGTTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC
TCAGGATCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCCTTCACGTCCGCACCTCTATCAAAGAT
GCCTTGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTTAAACC
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
GAAAATAA (SEQ ID NO: 370)

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT
 TCTTGGCATGATGGCATTGTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA
 5 ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
 TCATTTCCGATGTGAAATATTAGCTGTCCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
 TTATCACCATGGTGATATCAAATATGGCCTTCTCTGGTTCTTCCACTGATGGTCATTTTTTTC
 TCCTATATGTTTCATCCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
 CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTACGGTACCATCTTCTTT
 10 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATGCAAGCATTAGAC
 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT
 GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAAACCAATCACTA
 A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLVFGFTDYLPLRVTLFLVFLLVYTLTMVGNILLILVNINSSLQIPMYYFLSNL
 SFLDISCSTAITPKMLANFLASRKSISPYGALQMFFASFADAECILILAAAMAYDRYAAICNPLL
 YTTLMRRVCVCFIVLAYFSGSTSLVHVCLTFRLSFCGSNIVNHFFCDIPPLLALSCTDTQINQL
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
 20 YSLDTDKVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTCACAGATTATC
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCTTCTGGTATATACATTAAGTATGGTCGGA
 AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATCCCATGTATTATTT
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
 CTTCGCTTCTTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
 CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
 CATGTGTTGGCATATTTCAGTGGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
 30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT
 GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
 TCCAGACCAGCACTTTTGTGGTAATATTTTCTTACTTCTGCATCCTCATCACTGTGTTG
 AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATCTCCACTGTGCTTCCCACCTCATAG
 CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACCTATTCC
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA
 TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGAATAGTCAATATCTAA (SEQ ID NO:
 364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGVMVRHTNESNLAGFILLGFSDDYPQLQKVLFLVILILYLLTILGNTTI
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
 TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCMALASMAWLSGIATTLVQSTLTQLPFCGH
 RQVDHFICEVPVLKILACVGTTFNEAELFVASILFLVPVSFILVSSGYIAHAVLRIKSATRRQKAF
 45 GTCFSLTLVTVIFYGTIIFMYLQPAKSRSDQKGFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
 VLAKALGVNIL (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
 TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTTCTGATTATCC
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTGGGGA
 ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
 CTTTCTCATCTCTCCTTCTGTACCGCTGCTTCACCAGCAGTGTTATCCCCAGCTCCTGGT
 AAACCTGTGGGAACCCATGAAAATATCGCCTATGGTGGCTGTTTGGTTCACCTTTACAAC
 TCCCATGCCCTGGGATCCACTGAGTGCCTCTTGGCTCTGATGTCTGTGACCGCTATGT
 55 GGCTGTCTGCCGTCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
 CATCTATGGCATGGCTCAGTGGAATAGCCACCACCTGGTACAGTCCACCCTCACCTGCA

ATGGAAAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
CTGCAGGTTCCCCTCTTTATAACGTTCCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
GGGAATTATTGTATTGATATTCTGGGATTCCTGTCTCCACAATCCCATGTACTTTTTTCTCA
GTAACCTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACCTCCCATCGTCATGGCTGGA
5 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
TAGGCTCCTACCTCTGTGGTTTCCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTTGTGAGCTTCAATATCT
TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG
CACTCAGCTTCAAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCTCTGGTCTA
15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNSQSCVVEFILLGFSNYPELQGQLFVAFVLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
20 SVVDLSFSAVIMPEMLVVLSTETISFGGCFQMYFILLFGGAECFLLGAMAYDRFAAICHPL
NYQMIMNKGVMFKLIIFSWALGFMGLTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTF
FEIYAFGTFLIILVPFLLILLSYIRVLFALIKMPSTTGRQKAFSTCAHLTSVTLFYGTASMTYLG
PKSGYPETKKVMSLSYSLLTPLLNLLIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCTGTTATTTATCTGGTGACCCTGATAGG
AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
TTCTCCTGAACCTATCTGTGGTGGACCTGAGTTTCAGTGACGTTATTATGCCTGAAATGCT
30 GGTGGTCTCTCTACTGAAAAAATAACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTTGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTATGAAA
TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
35 TAGAAGTGCATGTGCAGACACGTTTTTGTGAAATCTATGCATTCACAGGCACCTTTTTG
ATTATTTGGTTCTTTCTTGTGATACTCTTGTCTTACATTGAGTTCTGTTGCCATCCTG
AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCATAT
CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
ACCGGAAACCAAGAAAGTGATGTCTTACTCACTTCTGACACCACTGCTGAATCTG
40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

15 MIVQLICTVCFLAVNTFHVRSSFDLKAADDMEINQTLVSEFLLGLSGYPKIEIVYFALILV
LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSVPSTLVSLISKRNISFSGCAVQ
MF GFAMGSTECCLLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSVQTLLAMRL
PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILYILQMN
SATG RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR
NKDVKAADVLYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTCAAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC
TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTCAGAA
TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTCTGGATATCTGCTAT
ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
 FIDVCYISSTVPKMLSNLLQEQQTITFVGCHQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV
 5 MTAILTMFFGIALSALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTA VSLFYTSGIFVYLRSSS
 GGSSSFDRFASVFTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
 TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
 10 TGGAACTCTCCCTCATTGTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
 CTTCTCAGTAACCTGTCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
 TCTCCAACCTCTTACAGGAACAGCAAATATCACITTTTGTGGTTGTATTATTCAGTACTTT
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
 ATGCTGCCATTTGTAACCCCTGCTCTATTCATCCATCATGTCAACCCACCTCTGTGTTTGG
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT
 TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCAACTGT
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGAGGTT
 CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTTGCAAAAGAGA
 AAGTGCTGCTGA (SEQ ID NO: 354)

25 **AOLFR192 sequences:**

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYILITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY
 TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPLTLSCSDNYISEM
 30 VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPEGRQKAFSTCASHLTA VSIIFYGTGIFMYLRPNSS
 HFMTGDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
 CTGCAGATCCCCTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCTCA
 35 GTAACTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
 GTTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTTCTTTG
 TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC
 ATTGTGTAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
 ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCTACTGGGAACACTTTTCAGGC
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTCTGTGATGCTCCTCCTCTCTTGACT
 CTCTCATGTTACAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
 ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCACCTTACTGCAG
 TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNP MYFFLSNLSLV
 50 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRYAAVCKPLHY
 TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCCKSNEVHHFFCDIPAVMVLSCSDRHISEL
 VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
 SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
 55 357)

AOLFR190 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
YAQTMPRRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ
5 AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPSSS
YSLKRDKMVSTFYTMLFPMLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
GGATGCAACTGGGCCTCTTTGTGGTGTTCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG
10 TAGACCCTCATCGTGTTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTTGTCA
TTGGAAATCTGTCAATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGAGTTCCTTCTCTGC
CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
15 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG
GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT
CCTTATACTATGGCTCCATTCTCTACAACTACTCCCGGCCAAGTCCAGCTACTCCCTCAAG
20 AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

AOLFR188 sequences:

MFPSLPCPVLLVQLPLMNENMQCFVFCSDSLLRMMVSRFIHVPFVKMKRIIVGGYSKHFFSN
 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCRRLHLSPTPSEEHMKNKNNVTEFILL
 GLTQNPEGQKVLVFTLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
 5 MIVDLLSEKKTISFQGCMAQLFMDHLFAGAENVLLVVMAYDRYMAICKPLHELITMNRVVCVL
 MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
 AVTFFTILLSYGVILHSLKTQSLEGKRKAFYTCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV
 VLTFTPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

10 ATGTTCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCACCTTATGAATGAGAACAT
 GCAGTGTGTTTGTGTTTCTGTTCTTGTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
 ATGTCCCATTTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
 TTTTGACATGGAGCTTCTGACAAAATAATCTCAAATTTATCACTGACCCTTTTGTGTTGTAGGC
 15 TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAATGTGACTG
 AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAGGTTTTATTTGTCACATT
 CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
 AGCCAGTCCCTGGGTTCCCCCATGTACTTTTTCTGGCTTCTTATCATTCATAGATACCGT
 CTATTCTACTGCATTTGCTCCCAAATGATGTTGACTTGCTCTCTGAGAAAAAGACCATT
 20 CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTTATTTGCTGGTGTGAAGTCATT
 CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA
 TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTCT
 TCACTCATGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
 ACAACTTCCTGTGTGATTTGTATCCCTTATTGAAACTTGCTTGCACCAATACCTATGTCACT
 25 GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTACCTTCTTCACTATCCTGC
 TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGGAAACGAAAAGC
 TTTCTACACCTGTGCATCCACGTCCTGTGGTCATTTTATTCTTTGTCCCTGTATCTTCTT
 GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA
 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
 30 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
 (SEQ ID NO: 348)

AOLFR189 sequences:

15 MQQNNVPEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKSSRTLGSMPYFFLFYLSF
 ADSCFSTSTAPRLVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
 TIMSQQVCILIVLAWIGSLIHSTAQILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL
 VNSGAICSSSFMIILISYIVILHSLRNHSAKGKKKALSACTSHIIVILFFGPCIFIYTRPPTTFPMD
 KMAVFYTGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

40 ATGCAGCAAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
 GGCAGAAAAATAGTGTGTTGTAATCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTAATCTTTCTA
 TTTTATTTGTCCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCATGATTAATTTGGA
 45 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
 CATTTATTTGGCTGCATGGAGATCTTTGTCCTCATTCTCATGGCTGTTGATCGCTATGTGGC
 CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
 GTTCTTGCCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
 GCCTTTCTGTGGACCCATTTGATTGATCATTATTGCTGTGATTGTCAGCCCTTGTTGAAAC
 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
 50 CTAAGTAGTTTCATGATTTTGATAATTTATATATTGTCATCTTGCACTCACTGAGAAACC
 ACAGTGCCAAAGGAAGAAAAAGGCTCTCTCCGCTTGACAGTCTCACATAATTGTAGTCAT
 CTTATTCTTTGGCCCATGTATATTATATACACGCCCCCGACCACTTTCCCATGGACA
 AGATGGTGGCAGTATTTTATACTATTGGAACACCTTTCTCAATCCACTCATCTACACATCT
 55 GAGGAATGCAGAAAGTAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAACATCCCCTGA (SEQ ID NO: 342)

5 **AOLFR186 sequences:**

MSNASLVTAFILTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAI SYPL
RYTSMMSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRRTSDGRRRAFQTCASHCIVVLCFFVPCVVIYLR
10 PGSDAMDGDVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLRDKVAHPQRK (SEQ ID NO:
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCTTCCCCATGCCCCAGGGC
15 TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCTGCGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
20 CCACCGGCACCTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCTGTAGTGTGCTCCTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCGCACCTCAGATGGGAGGCGCAGACGCTTTCAGACCTGTGCCTCCCACTGTATTGT
25 GGTCTTTGCTTCTTTGTCTGTTGTGCTATTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAACTTAGAGACAAAGTAGCACAT
CCTCAGAGGAAATAA (SEQ ID NO: 344)

30 **AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGPGLQLHIWLSIPFCIMYIAALEGNLILI
CVILSQAILHEPMYIFLSMLASADVLLSTTMPKALANLWLGYSHISFDGCLTQKFFIHLFIHSA
VLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
35 ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVIPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACCTCTGACACTCGCATAGCAGGCTGCTTCTCACTGGCATCCCTGGGCTGGA
40 GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCATCCTCTCCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGCTTGTCTCTACCAACCACCATGCCTAAGGCCCTG
GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAAGTTCTT
CATTCACTTCTCTTCACTTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
45 CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC
50 CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTCATTCTCCTATGCTCAAT
CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

55

ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTTATCACCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

5 AOLFRI84 sequences:

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTPLIAVYLLSALGNGTILWIALQPALHR
PMHFFLLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVFVSMESSVLLAMSID
RALAICRPLHYALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSFLVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF
10 YIPMILLALINHPITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNRLQPRKVGGAAQ
(SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC
15 TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTGCTTAGTGTGTCTGATATTGGATTGGT
CACTGCCCTGATGCCCACACTGCTGGGCATCGCCCTTGTGGTGTCTCACACTGTCCCTGCC
TCAGCCTGCCTTCTACAGATGGTTTTATCCATGTCTTTCTGTCTGTCATGGAGTCCCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
20 CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTCTTTTCGATGCCTGGGTCTCC
ATCTGCCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCCTCCACAGGTCTTAACCCAT
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCCAGAAGCTTGGGGTGCAGCCT
ACAGCCTATTTGTGGTTCTTTAGCCATGGGTTTGGACCCCTGCTTATTTCTTCTCTAT
GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
25 CAAACCTGTGCTGCCACCTCTCTGCAGTGTCTCTTCTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCTCCTCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
AAGAGAATACTCAACAGGTTGCAGCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
340)

30

AOLFRI85 sequences:

MFYPILNDISTKNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR
VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYFLAMLAITDLVLSSTQPKMLAIFWFAHEIQYHACLIQVFFIHFSSVESGVL
35 MAMALDCYVATCFPLRHSSILTPSVVIKLTIVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLVCAOTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYIPALFSFLTYRFGHDVPRVHILFANLYLLIPMLNPIIYGVRTKQIGDRVIQCCG
NIP (SEQ ID NO: 341)

40 ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTGATGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCCAATCACC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTTGTTTTGATTGTT
ATCATCTGCAGAGAGTAGATTGCGTTCCAGCAGAGACCATATTAACCAGTCCATGGTGCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTCTCATCCTGCTTGGAAATCCAGGCCTG
45 GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCCACTCAACCTAAGATGTT
GGCCATATTCTGGTTTCATGCTCATGAGATTCACTACCATGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC
50 GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTCTGTGATCAAAC
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCTTCTGCTTCATGGTGTC
TAGGATGCCCTTCTGCCAACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCTTCT
CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTCATACGTGATGATTTTGAGAGCTGT
55 GCTTCAGTTGCCCTCAGGTGAAGCCCGCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTGTCATCTTGGCTCTTTATATCCAGCCCTTTTTCTTCTCACCTACCGCTTTGGCCAT

GGGTCTTCTTGTTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCTTC
 ATTCATGGATTCACTGTCTATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
 TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG
 GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTCACCTTAAGGAG
 5 ATTAATAATATTGTCAAAAGAATCTTCTTCTCACTCATACTGTCTTCATCAGGATACCATGA
 AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT
 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
 TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGCTGTG
 CTCACCTTCTATGTGCCCATCATCACCCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
 10 GCCCTCTTGTTGTGATCCTTATTGCAGATATGTTCTTGTGTTGGTGCCGCCCTTATGAACCCC
 ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

15 MTLGSLGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
 SMLALIDLGLSLCTLPTVLGIFVWGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP
 LHYVSILTNTVIGRIGLVSLGRSVALIFPLPFMLKRFPCGSPVLSHSYCLHQEVMKLACADMK
 ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
 IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVIVSVKTKQIRDRVTHAFCY (SEQ ID NO: 335)

20 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCCTGCTGAGTG
 GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCCTGTGCTTCATGTATCT
 GGTTCCTATCCCGGGCAACTGCACAATTCTTTTATCATTAAAAACAGAGCGCTCACTTCAT
 GAACCTATGTATCTCTTCTGTCCATCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
 25 TCTCCCTACAGTCTCTGGGCATCTTTGGGTTGGAGCAGAGAAATTAGCCATGATGCCTGC
 TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTTCCTCGAGTCTCTGTGCTACTGTCTATG
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCTAGTGTAGCACTCATTTTCCATTA
 CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
 30 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
 GTTTGTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTTATGCTCTGA
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
 TGTTCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT
 35 CTTTCTCCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAAACAGATCCGGGATCGA
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

AOLFR183 sequences:

40 MTNLNASQANHRNFILTGIPGTPDKNPWLAFLPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFL
 SILALTDVSLSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGLVLSMAFDRFVAIRN
 PLHYVSILTHDVIRKTGISVLTRAVCVVFPVFLIKCLPFCHSNVLSHSYCLHQNMRLACASTR
 INSLYGLIVVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKTLSLHSMSTVLLFYVPFMGA
 ASMHRFWEHLSPVVHVMADIYLLPVLNPIVYSVKTKQI (SEQ ID NO: 337)

45 ATGACGAACTTGAATGCATCACAGGCCAACCCGTAACCTTCATTCTGACAGGTATCCCAG
 GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCCTGGGATTCTCTACACACTCACACT
 CCTGGGAAATGGTACCATCCTAGCTGTCTATCAAGGTGGAGCCAAGTCTCCATGAGCCCACG
 TATTACTTCCCTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTGATGCATGCATCATGCAGAT
 50 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCTAGTGTCCATGGCCTTTGAC
 AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTG
 AAAGACTGGAATATCTGTCCTACCCGGGCAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT
 ATAAAGTGCTACCTTCTGCCATTCCAATGTCTTGTCTCATTCACTGTCTTACCAAAA
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTGTG
 55 ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTACCCTGAAGAC
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCTCAGCACATGCCTCTCTCAC

ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC
 GGGAGATTCAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
 AACCTTGTCATTGTATTCACTGTAACCATGGATGCTCATCTGCACTCCCCATGTATTTCT
 5 CCTGGCTAACCTCTCAATCATTGATATGGCATTGTTGCTCAATTACAGCCCCTAAGATGATTT
 GTGATATTTTCAAGAAGCACAAAGGCCATCTCCTTTTCGGGGATGTATTACTCAGATCTTCTT
 TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
 TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA
 10 GATTTACCTTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
 CAGACTTGCCTGTACCAACACCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACTC
 ATTTCTGTGGGCTCCTTTGTCTTGTCTGGTAATTCCTACATCTTCATTCTGTTCACTGTTTG
 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCACTGTG
 GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT
 15 GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
 CATTGAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
 TTACAAAGATTTTGTA (SEQ ID NO: 330)

AOLFR180 sequences:

20 MTNKMAYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSNFLLTAFPGLECAHVWISIPVCCLYTI
 ALLGNSMIFLVIITKRLHKPMYYFLSMLAAVDLCLTITLPTVLGVLWFHAREISFKACFIQMF
 FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILDRMVLVIGLVICIRPAVFLPLLVAINTVSF
 HGGHELHPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGLDVLFILFSYVLILRTVLGIVARKK
 25 QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLPPVLNPIIYSLKTKTIR
 QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCCTCATAGT
 TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCCTCAAACCTTCC
 30 TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
 CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTTCATCATTACTAAGCGGA
 GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
 ATTACGACCTTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCCGGGAGATCAGCTTTAA
 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCTCCTCGGTGCTGG
 TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
 35 ACAGACAGGATGGTCTGCTGATAGGGCTGGTTCATCTGCATTAGACCAGAGTTTCTTAC
 TTCCCTTCTTGTAGCCATAAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
 TTTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT
 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTTCTCCTAT
 GTCCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAGCTCTCA
 40 GCACTTGTGTCTGTCACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
 TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA
 TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATCCGC
 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
 45 GGGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

MSVLNNSEVKLFLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMMYYFLAML
 AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
 50 YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
 IYGFIALCTMLDLALIVLSYVLILKTIISLASAERLKALNTCVSHICAVLTFYVPIITLAAMHHF
 AKHKSPLVVILIADMFLLVPLMPNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCCTTCTGATTGGGATCCCAGGACTGG
 AACATGCCACATTTGGTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC
 55 AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
 CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCTACCATGTTGA

AOLFR177 sequences:

MSFFFVDLRPMNRSATHIVTEFILLGFPGCWKIQIFLFLVYVLTLLGNGAIHYAVRCNPLLH
 TPMYFLLGNFAFLEIWYVSSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTECLFLAVMAYD
 5 RYLAICHPLQYPAIMTVRFCGKLVSFCLWIGFLGYPIPIFYISQLPFCGPNIDHFLCDMDPLMAL
 SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLLTAVFQVPSAAGRRAKAFSTCGSHLVVVSFLFYG
 TVMVVMYSPTYGIPTLLQKILTLVYSVTPLFNPLIYTLRNKDMKLALRNVLFGMRRQNS
 (SEQ ID NO: 325)

10 ATGTCCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
 AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTAGATTTCCTCTTCTCATTGTTT
 TTGGTGATTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
 ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTGCCTTCCTTGAGATCTGG
 TATGTGTCCTCCACTATTCCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
 15 ATTTTCTGGGTGCTTCTCCAGTTCTATTTCTTCTTTTCACTGGGAACAACTGAATGTCTCT
 TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
 CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTG
 GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCCTTCTGTGGTCCCTAATATCATTGAT
 CACTTCCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCATAACTG
 20 AATGTATTTTCTATACTCAGAGCTCCCTTGCTCTTTTCACTAGTATGTACATTCTTCGA
 TCCTATATCCTGTTACTAACAGCTGTTTTTCAAGTCCCTTCTGCAGCTGGTCGGAGAAAAG
 CCTTCTCTACCTGTGGTTCTCATTTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA
 ATGTATGTAAGTCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT
 ATTCAGTAACGACTCCTCTTTTAAATCCTCTGATCTATACTCTTCGTAATAAGGACATGAAA
 25 CTCGCTCTGAGAAATGTCTGTTTGAATGAGAATTCGTCAAATTCGTGA (SEQ ID NO:
 326)

AOLFR178 sequences:

MVGANHSVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
 30 ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
 LQYLTIMSPRMCMFFLVAAWVTGLIHSVVQLVFVVNLPFCGPNVSDSFYCDLPRFIKLACTDSY
 RLEFMVTANSFISLGSFFILIISYVVIIITVLKHSSAGLSKALSTLSAHVSVVVLFPGPLIFVYT
 PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)

35 ATGGTTGGGGCAAATCACTCCGTGGTGTGAGAGTTTGTGTTCTCCTGGGACTCACCAATTCCT
 GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTTACATGGCCAGTATGATGGGA
 AACTCTCTCATTTTGTCTACTGTGACTTCTGACCCTCACTTGCACTCCCCCATGTATTTCT
 GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAAATGATTT
 ATGACCTGTTTCAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
 40 CATCCACGTCATTGGCGGTGTGGAGATGGTGTGCTCATAGCCATGGCCTTTGACAGATAT
 GTGGCCATATGTAAGCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
 TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA
 AACTTGCCCTTCTGTGGTCCCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCT
 CAAACTTGCCCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTCT
 45 ATCTCTCTGGGCTCCTTCTTCTACTGATCATTTTCTATGTGGTTCATATTCTCACTGTTCT
 GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTAGCTCACGTCAGTGTG
 GTAGTTTTGTTCTTTGGTCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
 GGATAAGTTTCTGGCCATCTTTGATGCAGTCTCACTCCTGTTTTAAATCCTATCATCTACA
 CATTACAGGAATTGA (SEQ ID NO: 328)

50

AOLFR179 sequences:

MNGMNHVSSEFVFMGLTNSREIQLLLVFVSLFLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
 55 ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
 LHYLTIMSPRMCLYFLATSSIIIGLIHSLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
 EFMVTVNSGLISVGSFVLLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYT
 PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVMRRRLCSRLAHFTKIL (SEQ ID NO: 329)

TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGTT
CTTTGACATCAAGACTTGGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

5 AOLFR175 sequences:

MHFLSQNDLNNLPHLCLHRHSVIAGAFTIHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
SGCFLQFYFFFSLGSTECFFLA VMAFDRLAICRPLRYPTIMTRRLCTNLVVNCWVLGFIWFLIPI
VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVVRVL
10 RVPSAAGRRAKAFSTCGSHLAVVSLFYGSVLV MYGSPPSKNEAGKQKTVTLFYSVVTPLLNPVI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
TCATTCAAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
15 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGGAGATATGTTATGTACCTCCACAGTCCCCAGCATGCTGGCCAACTTC
CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCTCCAGTTCTACTTTTTCTTCTCC
20 TTGGGCTCTACAGAATGCTTTTCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG
TCGGCCTCTACGCTATCCAACCATTATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCTATCGTCAACATCTCCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC
25 TCTTTCTCTTCATTGTGGGGTCTATGCTCTGGTCTGTGAGAGCTGTGTTGAGGGTCCCTTCA
GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCAACATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTATTCTGTTGTTACCCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:
30 322)

AOLFR176 sequences:

MFFIIHSLVTSVFLTALGPQNRMTMHFVTEFVLLGFHGGQREMQSCFFSFLVLYLLTLLNGAIVC
AVKLDRLRHTPMYILLGNFAFLEIWIYSSTVPMNLVNILSEIKTISFSGCFLQFYFFFSLGTTTECFF
35 LSVMAYDRYLAICRPLHYPSIMTGKFCIHLVCVCWVGGLFCYPVPIVLISQLPFCGPNIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSNGPMQKJITLVYTAMTFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

ATGTTCTTTATTATTTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTATCCTGGTTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCAGTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA
AACTTTGCCTTTCTAGAGATCTGGTACATTTCTCCTCACTGTCCCAAACATGCTAGTCAATAT
45 CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTCT
ACTGGGTACAACAGAGTGTTTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCAACTTCCCT
TCTGTGGGCCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCATTGTTTGCAGTGGC
50 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTCTGGTCAACTAAAGCTTTCTCCACATGTGGGTCCCACCTAATGGTGGTGTCTC
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACAGCAATGACTCCATTCTTAAATCCCCTTATCTAT
55 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
ACCCATTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
5 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA
ACTTTCCCTTTGATAAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTTATTCTAGTTCTA
AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

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AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
FLLAILAATDLGLATSIAPGLLAVLWLGPRSPYAVCLVQMFFVHALTAMESGVLLAMACDR
AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV
15 VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSHICVIL
AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPLNPLIYGARTKQIRDRLLETFTFRKSPL
(SEQ ID NO: 317)

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ATGGCAGAAACTCTACAACCTCAATTCCACCTTCTACACCCAACTTCTTCATACTGACTG
GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTATCT
GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
CCAGCCCATGTTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCCTGGTCACC
AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA
TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG
30 GTACATGTAGTTCTCACATCTGTGTCTATTCTGGCCTTCTACATACCTGGTCTCTTCTCTAC
CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC
AGAGACCGACTCCTGGAAACCTTCACATTAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

AOLFR173 sequences:

MSHTNVITIFHPAVFVLPGIPGLEAYHIWLSIPLCLIYITAVLGNSILIVVIVMERNLHVPMPYFFLS
MLAVMDILLSTTTVPKALAIFWLQAHNIAFDACVTQGGFVHMMFVGESAILLAMAFDRFVAIC
APLRYTTVLTPVVGRIALAVITRSFCIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
40 NIWYGFSVPIVMVILDVILIAVSYSILRAVFRLPQDARHKALSTCGSHLCVILMFYVPSFFTL
THHFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSPLGS
(SEQ ID NO: 319)

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ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTCCTGGCATCCCTGG
GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTGCCTCATTTACATCACTGCAGTCC
TGGGAAACAGCATCCTGATAGTGGTTATTGTCTATGGAACGTAACCTTCATGTGCCCATGTA
TTTCTTCTCTCAATGCTGGCCGTGATGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
CCCTAGCCATCTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCCAAGGC
TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
50 CTTTGTGGCCATTTGTGCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
AGGATTGCTCTGGCCGTATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCCCTCACTCCTACTGTGAGCATATTGGA
GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTGGTATGGCTTCTCAGTGCCCAT
TGTCATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
55 TGTTTCGTTTGGCCTCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCCACT
CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG

GGATTGCTCTTCCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG
 TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
 AACCTTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
 CATGGGTGTTTGGATTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC
 5 CGCAAATCAAATTCATTAGACCATTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCCT
 GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTATTCTCATTGGT
 TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
 AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACCTGTGTTGTGATTG
 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA
 10 TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTACTCT
 TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
 GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:

15 MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS
 ASPSVFCFSMCGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI
 ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDDLVPKHVITFTGCMVQFYFHFSLGSTSFLIL
 TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
 FFCNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLRIPASSCQKAFSTCG
 20 SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTPLNPFILTFCNQTVKTVLQGMQ
 RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACCTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCTGTTTGT
 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCTTT
 25 CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTC
 TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTCTTGATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCTTCTCATGCTTATCTTCTCGCCTTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
 30 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCCAGGATGCTCT
 CAGACCTGTTGGTCCCCCAAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCTGACAGACATGGCCCTTGATCGCTTTGT
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTTCCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC
 35 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
 TGTCTCAGCTCCTTCTGCTGACCCCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACACT
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTGAGGCTGGCAAAGCTCACTCT
 40 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTACCCCCCTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTTAAACAGTGCTACAGGGGCAGATGCAGAGGCT
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

45 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAISTAMSPKLMIDLLCDKIAISLSACMGQLFI
 EHLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMAMIGGFVHSVQIVFLYSLP
 ICGPNVIDHSVCDMYPLLELLCLDTYFIGLTVVANGGIIICMVIFTLLISCGVILNFLKTYSQEER
 HKALPTCISHIIVVALVFVPCIFMYVRPVS NFDFDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM
 50 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

ATGGTGGGAAACCTCCTCATTGTTGGGTGACTACTATTGGCAGCCCCCTCTTGGGCTCCCTAA
 TGTACTTCTTCTTGCCTACTTGTCACTTATGGATGCCATATATCCACTGCCATGTACCCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC
 AGCTCTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCTTTTGGTGGTGATGGCCTA
 55 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT

FVYLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID NO: 307)

5 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTACTTCTTCTTAAGCAACTTATCTTTTATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC
AGTTTTTTTTCTTTGTGGCATGGGTCTGTCTGAGTGCCCTCCTGACTGCTATGGCATAAC
10 GACCGATATGCAGCCATCTCCAGCCCCCTTCTTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTGCAGGACCCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCTGGCTCTGTCTGTGCTCTGACACCTTCCTCAGTCAAGTGGTGAATTTCCCTCGTG
GTGGTCACTGTGCGAGGAACATCGTTTCTCCAACCTCCTTATCTCCTATGGTTACATAGTGT
15 CTGCGGTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTTCGTGTAATTTGCGACCCAG
CTCCAGCTACTTGCTAGGCAGGACAAAGTGGTGTCTGTTTTCTATTCAATGGTGATCCCC
ATGCTGAACCCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTTTCTTAG (SEQ ID NO: 308)

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AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCFVVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMA YDRYVAICKPLHYM
TIMNRETCKMMLLGTWVGFLSHIQVALVQLPFCGPNEIDHYFCDVHPVLKLACTETIYVG
25 VVV TANS GTIALG SFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRP
TTFSEDKMVA VFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO:
309)

30 ATGGAAAAATAAACAACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTGTTTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG
CTTCTTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTTATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
35 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGTGTTGAAA
CTTGCCTGCACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
40 CAGTCAGCAGAAGGCAGGCGCAAAGCCTCTCCACCTGTGGCTCCACATTGCCATGGTGC
TTATCTTTTTCGGCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

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AOLFR169 sequences:

MMDNHSSATEFHLLGFPGSQGLHHILFAIFFFFYLVTLMGNTVIIIVIVCDKRLQSPMYFFLSHL
STLEILVTIIVPMMLWGLLFLGCRQYLSLHVS LNFCGTM EFALLGVMAVD RYVAVCNPLRY
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLLKLSCDNTLLTEFI
50 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCTGGGTCCCAAG
GACTACACCACATTCTTTTGTCTATATTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC
55 ACGGTCATCATTTGTGATTGTGTGTGGATAAACGCTCTGCAGTCCCCCATGTATTCTTCTCCT
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
 SNLSFLDICYVSSSTAPKMLSDIITEQKTISFVGCAQYFVFCGMGLTECFLLAAMAYDRYAAICN
 PLYTVLISHTLCLKMVVGA YVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
 5 TSEVVTFIVSVVGVSVLVVLISYGYVA AVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
 YMRPSSSYSLNRDKVVSIFYALVIPVVPNIYISFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
 (SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTTCAGACC
 10 ATCCTCAAATGAAGATTTTCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
 TGGAACCTTAAGCCTCATTGCCCTCATTAAGATGGACTCTACCTGCACATGCCCATGTACT
 TCTTCCTCAGTAACCTGTCCTTCTGGACATCTGCTATGTGTCTCCACCGCCCCCTAAGATG
 CTGTCTGACATCACAGAGCAGAAAACCATTTCTTTGTTGGCTGTGCCACTCAGTACT
 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
 15 GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACACTTTGTTTAA
 AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTCATTGAAACATACTCTGT
 CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTTCTGTGACCTCCCTCCAG
 TCCTGGCTCTGTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT
 20 TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
 ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCAGCTA
 CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT
 CCCATCATCTACAGTTTATAGGAATAAGGAGATTA AAAATGCCATGAGGAAAGCCATGGAA
 AGGGACCCCGGATTCTCACGGTGGACCATTATTTTATGACCTTGGGCTAA (SEQ ID
 25 NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVS LVLFLLLVYVTTLLGNLLIMVTVTCE SRLHTPMYFLLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFQMF LFLHIGGVDFVSL SVMALDRYVAISKPL
 30 HYATIMSRDHCIGLTVA AWLGGFVHSIVQISLLLPLFCGPNVLDTFYCDVHRVLKLAHTDIFIL
 ELLMISNGLLTTLWFFLLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCYVYARP
 FTALPMDKAISVTFTVISPLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAACTGCACCAGGGTAAAAGAATTTATTTTCTTGGCCTGACCCAGAATC
 35 GGAAGTGAGCTTAGTCTTATTTCTTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTTT
 GCTCCATAATTTATCTATTGCCGATATCTGCTCTCTTCCATCACAGTGCCCAAGGTTCTGG
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
 40 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCTGTTGCTC
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCTT
 CAACTGGCCCATACAGACATTTTCATACTTGAAC TACTAATGATTTCCAACAATGGACTG
 CTCACCACACTGTGGTTTTCTGCTCCTGGTGTCTACATAGTCATATTATCATTACCCAA
 45 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACTGT
 GGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCA
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

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AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLQALLFVTF LGIYLLTLAWNLA LIFLIRGDTHLHTPMYFF
 LSNLSFIDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFVGMGLSECLLLTAMAYDRYAAI
 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNINHFFCDLPPVLALSCSDT
 55 FLSQVVNFLVVVTVGGTSFLQLLISYGYTVSAVLKIPSAEGRWKACNTCASHLMVVTTLLFGTAL

GTGTATCTTCATTGCCGCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT
GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
ATAATCCCTGTGCTAAATCCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
5 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN
LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
10 LYAQAMSIKLCALLVAVSYCGGFINSIITKKTFSNFCRENIDDFCDLLPLVELACGEKGGYK
IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFTSCSSHLTSVTLYYGSILYIYALPRS
SYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA
15 GGAATGCAGCTGGGCCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
ATAGACCCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
ACTGGAAATCTGTGTTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCACTTCTTCTTCT
CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
20 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTCAATCATCACCAAGAAAACGTTTTCT
CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTGCTTCCCTTGGTGG
AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
TGTCATCTGCCCCGAGTGCTCATCCTGGCCTCCTACCTCTTTATCATCACCAAGTGTCTTGA
25 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT
GTCACCTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAAGCTTCTCCCATAA (SEQ
ID NO: 300)

30

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHFFCELSSLISLSYPDSYL
35 SQLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPSASGHRKVFSTCASHLTAITFIHGTLFLYCV
NSKNSRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKINTKYFHIKHRHWYFPNFVIEQ
(SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
40 ATTACCTGGAAGTCAAATCCCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTGATEATCAAAATTAACCCAAAATTGCATACCCCATGT
ATTTTTCTCCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCCTCCATCATTTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGAATT
CTTTTTCTTTTGCACCTTTGTAGTGACTGAATTAATTCTATTGCGGTGATGGCCTATGACC
45 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCAGAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
TTTTAATGAGATAAGCACACTACTCATCTGACATCTTATGCATTTCATTGTCAACCA
50 CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCCTCCACCT
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTACACCGTGGTGATCCCCTTGTTGAA
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
ACAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTGTTATTGAACAATA
55 A (SEQ ID NO: 302)

TTGTCTTGT TTTTGTGCTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
GTGGCCATTTGTACCCCCCTTAGATACACAGTCATCATGAACCCCCGCCTCTGTGGCCTGC
TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG
AGGCTGTCCTTCTGCACAGACCTGGAATCCCGCTCTTCTTCTGTGAACTGGCTCAGGTCA
5 TCCAACTCACCTGTTTCAGACACCTCATCAATAACATCCTGATATATTTTGCAGCTTGCATA
TTTGGTGGTGTTCCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
GAGAATGCCATCAGCAAGTGGAAAGCACAAAGCAGTTTCCACCTGTGGGCTCACCTCTCC
ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
10 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTGAGGTTTCTAGAGTAA (SEQ ID
NO: 294)

AOLFR161 sequences:

15 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLMVMVGNLLIILAISIDSHLHTPMYFFLANL
SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH
YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
IFILIVAGMVIATPFVILASYARILVAIMKVPSAGGRKKAFSTCSSHLSVVALFYGTTIGVYLCF
SSVLTIVKEKASAVMYTAVTPMLNPFYSLRNRDLKGALRKL VNRKITSSS (SEQ ID NO: 295)

20 ATGGAACCAAGAAACCAAAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTTCT
TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
25 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC
TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCCTG
CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
30 TCCGACTTTCTGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
GGTGATAGCCACGCCCTTTGTCTGCATCTGCGCTCCTATGCTCGCATCCTTGTGGCCATCA
TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC
TGTGGTTGCTCTCTTCTATGGGACCACCATTGGCGTCTATCTGTGTCCCTCCTCGGTCCTCA
CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
35 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
AAAGATCACCTCATCTTCTCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

40 MMRLMKEVVRGRNQTEVTEFLLGLSDNPD LQGVLFALFLLIYMANMVG NLMIVLIKIDLCLH
TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
YDRYAAIWNPLLYPVLVSGRICFLLIATSF LAGCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPL
LKLSGSDTHFNGIVIMAFSSFIVISCVMI VLISYLCIFIAVLKMP SLEGRHKAFSTCASYLMAVTIF
FGTILFMYLRPTSSYSMEQDKVVS VFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
NO: 297)

45 ATGATGAGACTTATGAAAGAGGTTGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAGATTGATCTCTGT
50 CTCCACACCCCCATGTATTTCTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
GATGTGCTGCCAGTTCTACTTCTTTGGCTCCTTCTGAGGACTGAGTGCTTCTGTTGGCC
ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCCTGCTCTACCCAGTTCTCGTGT
CTGGGAGAATTTGCTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
CATACATACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTCT
55 ACTGTGACACCCCCGCACTGCTCAAACCTCTTGCTCTGATACCCACTTCAATGGCATTGTG
ATCATGGCATTCTCAAGTTTTATTGTCATCAGCTGTGTTATGATTGTCTCATTCTCCTACCT

5 ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTGAGGGGATC
 CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG
 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACACCCCCATGTACTTCC
 10 TCCTCTCTATCCTGTCCTTGGTCGACATCTGTTTACCTCCACCACGATGCCAAAGATGCTG
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
 TTGTCCTGGTTTTTGTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT
 TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGCT
 15 ACAGCTGACCTTCTGCATAGACCTGGAAATTCCTCACTTTTCTGTGAAGTAGCTCATATTC
 TCAAGCTCGCCTGTTCTGATGTCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
 GTTAGGTGTTGTTCTCTCTCTGGGATCATTTTCTCTTACACACGAATTGTCTCCTCTGTCA
 TGAATAATCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT
 CGTTGTTTCTCTTTTATGGAAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
 20 CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
 ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
 GATACCATCTTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

20 MGRNQTA VSEFLLMKV TEDPELKLIPFSLFSLMYLV TILGNLLILLAVISDSHLHTPMYFLLFN
 LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHPL
 RYTVLMNVHFWGLLILLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKACSDTL
 INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS
 25 SAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

30 ATGGGACCCAGAAACCAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAAGCTGAAGTTAATCCCTTTCAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAAGATCCT
 35 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCCAGATCTGT
 CTTGTCTTGGTTTTTGTGGCTTGGAAAGTTGCTTTCTTGCAAGTCATGGCCTACGACCGCTA
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
 GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTCAAGTC
 40 ATCAAGCTCGCCTGTTCTGACACCTCATCAACAACATCCTCATATATTTTGAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTCTCTTATTCTCAAATAGTCACCTCTGTTC
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTACCTCTC
 TGTCTTTCTCTTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
 CTTCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 45 CTTCTCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG
 GCTGTTTCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

50 MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFSLMYLV TILGNLLILL
 AVISDSHLHTPMYFLLSNLSFLDICLSTTTPKMLVNIQAQNSITYSGCLTQICFVLFAGLENC
 45 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLILLSLLTSVFNALLLSLMVLRSLFCTDLEIPLFF
 CELAQVIQLTCSDTLNNILIYFAACIFGGVPLSGIILSYTQITSCVLRMP SASGKHKA VSTCGSHL
 SIVLLFYGAGLGVYISSVVTDSPRKTA VASVMYSVFPQMVNPFYSLRNKDMKGTLRKFGRIP
 50 SLLWCAICFGFRFLE (SEQ ID NO: 293)

55 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAACTGCAGCCCGTCTTTTTCAGCCTGTTCTGTCCATGTACTTGGTCACCATCCTGGG
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT
 60 TCCTCTCCAATCTCTCTTTTGGACATTTGTTTAAGCACAACCACGATCCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIINDNLLIFSAVRL
 DTHLGNPMYNFISIFSLEIWTATIPKMLSNLISEKKAISMTGCILQMYFFHSLENSEGILLTT
 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIHQIFCDLVP
 5 VLSLACTDTSMILIEDVIHAVTIIITFLIILSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
 SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIHYSRLNKDMNNAIKKLFCLQKVLNKP GG
 (SEQ ID NO: 285)

ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
 10 ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
 CCTGTACTTCTTTCTTTACTTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
 CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
 CCTTTCTGGAGATCTGGTACACCACACCCATTCCCAAGATGCTCTCCAACCTCATCAG
 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTGCAGATGTATTCTTCCACTCACTT
 15 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
 ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGTTCC
 TGCCTCTTCGGTTTCTTATCCTGCTTCCCGAGATTGTGATGATTTCACACTGCCTTTCTG
 TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTCATGCTGTGACCATCATCATTACCT
 20 TCCTAATCATTGCCCTGTCCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT
 GAAGGGAGGCCAAAAGGCTNTTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
 TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC
 AGCCATTGCACTGATGTTTACTGTACTTGCCTTCTTCAATCCCATCATTTATAGCCTGA
 GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGAACA
 25 AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTA VFQFLIGISNYPQWRDTFFTLVLIYLSLTLGNGFMIFLIHFDPNLHTPIYFFLSNL
 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
 30 LRYSVVMNGPVCVCLVATSWGTSVL TAMLILSLRLHFCGANVINHFACILSLIKLTCSDTSL
 NEFMILITSIFTLPLPGFVLLSYIRIAMAIIRISLQGRKAFITTCGSHLT VVTIFYGSAISM MYMKT
 QSKSSPDQDKFISVFY GALT PMLNPLIYSLRKDV KRAIRK VMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTTCAGTTTCTCCTTATTGGCATTCTAACTATCC
 35 TCAATGGAGAGACAGTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
 AATGGATTTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
 CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
 TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC
 TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
 40 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTTATGAATGGCCCAGTGTGTGTCTGCTT
 GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
 CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTA
 GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCAACC
 TGCTGCTACCATTTGGGTTTGTTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG
 45 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
 TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCCCTCCCC
 TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
 ATATATAGCCTGAGAAAAAAGATGTTAAACGGGGCAATAAGGAAAGTTATGTTGAAAAGG
 ACATGA (SEQ ID NO: 288)

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AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLMLFLSMYLATMLGNLLIILAVNSDSLHHTPMYFLLSI
 LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
 LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFFCEL AHILKLACSDVLIN
 55 NILVYLVTSLGVPVPLSGHFSYTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLSS
 GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDMMLKALRLKISRIPSFH (SEQ ID NO: 289)

ATAGTCACTTTGTTTTATGGAACCCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTGAGCCCAATGCTGAACCC
ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

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AOLFR152 sequences:

MDQINHTNVKEFFLELTRSRELEFFLVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
KSVLDIVFSSITVPKFLVDLLSDRKTISYNDCAQIFFHFAGGADIFFLSVMAYDRYLAIKPL
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
10 FALELFMISNGLVTLWFLLLLSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV
YIYCRPFMTLPMDDTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLGPSERKWWG (SEQ ID
NO: 281)

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ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC
GAGAGCTGGAGTTTTTCTTGTGTTGTGGTCTTCTTGTGCTGTGTATGTAGCAACAGTCCTGGG
AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCTACACACTCCTATGTACTTTC
TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG
GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT
TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
CTTGCAATCGCCAAGCCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCATTCAATCATCCAGGTAATTCTGATGC
TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
GTAACAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
TGGTGACCCTGCTCTGGTTCCCTCCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG
AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG
GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCATGCTGAACCCCATCATC
TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

AOLFR153 sequences:

MSKTSLVTAFLTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAI SYPL
RYTSMMSGSRCALLATSTWLSGSLHSAVQTILTFHLPYCGPNQIQHYLCDAPPILKLACADTSA
35 NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFIYLR
PGSRDVEDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:
283)

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ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCACTCTTTGGAATCTTCTGCTGGTGTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCA
CCAACCTGTCTTTCATTGACATGTGGTTCCTCACTGTACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACAGATCCAGCACTATTGTGTGATGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
GGCCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
GGTCTTTGCTTTTTTGTNNCCTGTGTTTTTCACTTACCTGAGACCAGGCTCCAGGGACGTCG
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
TCTCAGGGAGAATAA (SEQ ID NO: 284)

TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT
TTCATTCTAGGGGGCACCAGTGTTCCTCTACAGGGTGCATGTCCTGTGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC
5 ATTTGCCCTACTGTGGACCCAAGTGGATCCAGCACTATTGTGTGATGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTGTGACTGTTGGAATA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGTGCTGCTATGTGTCCATCGTCTGTTCCATCTC
GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACCTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGAAAGC
10 TGTGGATGGAGTTGTGGCCGTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGT
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

AOLFR150 sequences:

15 MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTLLGNLLIMVTVTCESRLHTPMYFLLR
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSCMTQIFLHLLGGADIFSLVMAFDCYMAISKPL
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGRRKAISTCTSPHHCGBPFCALHCLC
PALHCPPHRKGHLCHLHCHLPSAEPDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

20 ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
AAGACCAGAGTTTGGTCTTGTCTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA
AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCATGTACTTCCT
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAAGTCTCTAAAGTCTTGC
25 TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTGTACTGCTACA
TGGCCATCTCAAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
CTCTCCCTTTCTGTGGACCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC
30 AAACCTCACTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTCCAACAATGGCCTGGT
CACTACCCTGTGGTTTATCTTCCCTGTGTGTCTGCTACACAGTCATCCTAATGACGCTGAGGT
CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTGCACTCCCATCACTACTGTG
GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC
AGAAAAGGCCATCTCTGTACCTTCACTGTCTCTCCCTCTGCTGAACCCTTTGATCTACA
35 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

40 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLLITLAGNLCMILLRTNSHLQTPMYFFLGHL
FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMLDRYVAICSPLHYS
SRMSKNICVCLVTIPYMYGFLSGFSQSLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA
MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTFLFCMYVRPPSE
KSVEESKITA VFYTF LSPMLNPLIYSLRNTD VILAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

45 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGGCATCTACCTAATCACACTGGCAGG
CAACCTGTGCATGATCCTGTGATCAGGACCAATCCACCTGCAAACACCCATGTATTTCT
TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
50 GCACAATTTCTCTCAGAACAGAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT
CTCTTCATCGCCCTGGTGTCACTGAGTTTACATCCTTGTCTCAATGGCATTGGATCGCTA
TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
TCACCTATCCTTCTGTGGCTCCCTTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
55 TAATCTCTCAAGCTCTCTCTTCATCATTCTCTGTCTATCTTTTCACTTTTGCAGCGATCTT
CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCACCTGACA

LAHREFGHNVSRTFHMIFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO: 271)

5 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCTTCAT
TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATCCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGCC
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTCC
10 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAAATTTGTCCTGGATTTCAGCCATTCTG
ATGGCCATGGCATTGTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATAACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGCTGACATGCCTGCCTTCTGCAGGACACGCATCATACCCCA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
15 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCTCCT
ACGCACACATCCTCTGTGCTGTCTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACCTGTGGTCTCATGTCTGTCTCATCCTCATGTTTTATACACCTGCCTTTTCTCCA
TCCTCGCCCATCGCTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
GAGATAAGGTTATACCTTTGTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

20

AOLFR148 sequences:

MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYFLC
MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCTQLFFIHSTFISESGILLVMAFDHYIAICYPLR
YTTILTALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG
25 FSILMSTVVLVDVLFISYMLILHAVFHMPSPDACHKALNTFGSHVCHILFYGSGIFTILTQRFRGR
HIPPCIHIPLANVCILAPPMLNPIIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

30 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCTTCATTTCTATGTCACCGCCCTT
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCTCTGCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
35 ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCCTTACAAATGCTCTGATCAA
GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATCCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTGGTATGGGTTTTCATTCTA
ATGTGACGGTGGTCTTAGATGTTGTACTAATTTTATTTTCTATATGCTGATTCTCCATGC
40 TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
TCTGCATCATCCTCTTTTATGGGTCTGGCATCTTCAACATCCTTACCCAGAGGTTTGGA
CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

45 **AOLFR149 sequences:**

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYYFLTNL
SFIDMWFSSTVTPKLLMTLVFSPGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWIQHYLCDAPPILKLACADTS
AIETVIFVTGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFTQCASHCIVVLCFFGPGLFIYLR
50 PGSRKAVDGVVAVFYTVLTPLLNPVYVTLRNKEVKALLKLKDKVAHSQSK (SEQ ID NO: 275)

55 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCTCA
CCAACCTGTCGTTCAATTGACATGTGGTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTSTFPGLEGIKHWIFIPFFFMVMVAISGNCFILIIKTNPR LH
 TPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
 RFVAICHPLRYSVIITGQQVVRAGLIVIFRGPVATIPVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
 5 CTDTTFNNLYGLMVVVFVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
 FVPMMLGLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK
 (SEQ ID NO: 267)

ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
 10 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC
 CCTTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
 ACCAACCCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTTCATGGAGTC
 15 CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCTCTGAGGTATT
 CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
 TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACTT
 CAATAATCTGTATGGACTGATGGTGGTAGTTTTCACTGTGATGCTGGACCTGGTGCTCATC
 20 GCACTGTCCTATGGACTCATCCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
 GCCGTGCCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
 ATGGGGCTGTCCCTGGTGCACCGTTTTGGGAAGCATGCCCCACCTGCTATTCTTCTTAT
 GGCCAATGTCTACCTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC
 AAGGAGATCCACCGTGCCATTATCAAACCTCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
 25 ID NO: 268)

AOLFR146 sequences:

MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVYLFSLM
 30 LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFLHGFSFMESSVLLAMSVDYVAICCP
 LHYASILTNEVIGRTGLAIHCCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
 SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYPMVGVSM T
 HRFKASPLVHVIMANIYLLAPPVMNPITYSVKNKIQWGMNLNLSLKNMHSR (SEQ ID NO:
 269)

ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 35 GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
 ATGGGCAATACCACCATCTCACTGCTCATTGCGCACAGAGCCATCTGTCCACCAGCGCATGT
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACTACCCACA
 GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAGAATCAGCTCTGAGGCCTGTTTTGCTCAGTT
 40 TTTCTCTCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCTCCTGGCTATGTCCGTTGACT
 GCTATGTGGCCATCTGCTGTCCCCTCCATTATGCCTCCATCCTACCAATGAAGTCAATTGGT
 AGAACTGGGTTAGCCATCATTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
 CAAGCGACTGCCTTTCTGCCACTCCCACTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTTGCTCTTGCTT
 45 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTATTCTGAAAAATA
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
 TCTAGCTGTCTCCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
 50 GATGAACCCCATCATTTACAGTGTAAAGAACAAGCAGATCCAATGGGGAATGTAAATTTCT
 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNCLLYLIVVEHSLHEPMF
 55 FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLD SAILMAMAFDHYV
 AICSPLRYTTLTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
 NFWYGFCVPIMTVISDVILIAVSYAHILCAVFLPSQDACQKALGTCGSHVCVILMFYTPAFFSI

AOLFR143 sequences:

MLGLNGTPFPQATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMYYFL
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 5 HVNNIYGLLVIIIFTYGMDSTFILLSYALILRAMLVIIISQEQRLKALNTCMISHICAVLAFYVPIIAVS
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTEIRKGILKFFHKSQA (SEQ ID NO:
 263)

ATGCTGGGTCTCAATGGCACCCCCCTTCCAGCCAGCAAACTCCAGCTGACAGGCATTCCCTG
 10 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTTTTGGGAGCCTGCTCTGCATCAGCCCATGT
 ACTACTTCCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCCTTTTCTACACTTCCCACT
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 15 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACTCTCTTCCCTTTCCCTTTTGTGGT
 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA
 TTTTACCTATGGTATGGACTCAACTTTCATCCTGCTTCTACGCATTGATCCTGAGAGCC
 20 ATGCTGGTCATCATATCCCAGGAACAGCGCTCAAGGCACCTCAACACCTGCATGTCACACA
 TCTGTGCAGTGTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTACCGCTTCTGG
 AAAAGTGCTCCACCTGTTGTTTCATGTCAATGTCTACCTGTTTGTACCAACCCAT
 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

25

AOLFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPCLVMYAVALGGNTVILQAVRVEPSLHEPMMYYFL
 SMLSFSDDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
 PLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
 30 NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
 TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA
 GAGCTCTCACTCCTGGCTGTCAGGGCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
 35 AATACAGTGATCCTGCAGGCTGTGCGAGTGAGCCAGCCTCCATGAGCCCATGTACTACT
 TCCTGTCCATGTTGTCCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
 CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTGAGATGTTTCT
 TATCACTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
 TGGCCATTTGTGACCCCTTGCGCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
 40 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG
 AGGCTTGCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTGTCTGTATCCAC
 CTTTGGCATGGACCTGTTTTTATCTTCTCTCCTATGTGCTCATTCTGCGTTCTGTATGG
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTACATATCCTGGC
 45 TGTACTTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGACCGCTTGGGAAGCAT
 GTCCCATGTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA
 CCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTCAC
 CACATCAAAATATGA (SEQ ID NO: 266)

CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAACTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

5 MLTLNKTDLIPASFILNGVPGLEDLQLWISFPFCSMYVVMVGNCGLLYLHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVMLMALDRYV
AICYPLRYSTILNPNVIAKVGTAFTLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFIDLITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
10 FSFFSHRFGHEHPPSCHIIIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ
ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG
GACTGGAAGACACAACTCTGGATTTCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG
15 TACTACTTCTTGGCCATGCTTTCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGCCAG
ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
GCAAAGGTTGGGACTGCCACCTTCTGAGAGGGGTATTACTCATTATTCCTTTACTTTCTT
20 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCC
ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG
25 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
CCCACTATGAACCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCATAA
GGATCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

30 MSSTLGHNMESPNHTDVPDSVFFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVL
HKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCEMESTVLLAM
AFDRYVAICHPLRYATILDTIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
VILISYTPALFSFFTHRFHGHVPHIHLANVYLLLPALNPVYGVKTKQIRKRVVRVFQSGQ
35 GMGIKASE (SEQ ID NO: 261)

ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
TCTTCTTCTCCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
40 AACCAGTCTTGACACAAGCCTGTGTACCTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTATGCCTTCTGCATGATGGAGTCCACT
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
45 GCTCATGCTCCCATGTCCCTTCTTATTGGGCGTTTGAAGTTCTGCCAAAGCCATGTGATCC
TACACACGTAAGTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACAGGCTTA
ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCAATTGG
TCTCTCCTATGCCCTAAGTGCACAAGCTGTCTTCTCGCTCTCATCCCATGAAGCTCGGTCCA
AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTATCCTCATCTCTTATACACCAGCCCTC
50 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGGC
CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAC
AGATCCGTAAAAGAGTTGTCAAGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
CTGAGTGA (SEQ ID NO: 262)

55

GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC
 TGGTGGCTGGGTCTGGGTTCATCGCTTGTGCGTGTGCTCTTTTGCATACCCTCCTCGGCC
 CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGGCCTGCT
 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
 5 GCCATTATGCTTCCATTCCCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
 CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
 GTGGTGAATATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
 CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACTCTTGAGTAGG
 10 TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACCTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
 FVDVWFSSNVTPKMLENLFSKKTISYADCLAQCFFIALVHVEIFILAAIAFDRTVIGNPLLY
 15 GSKMSRQVIRLITFPYIYGFLTSLATLWYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY
 TMLILAGINFTYSLTVIISYLFILAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
 ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

ATGCTCAATTTACCCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGGGAAT
 20 GGCAAGTCTCTTCTTCATCGTTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
 GGCATGATGTTGTTAATCAAGGTCAGTCTCAGCTTAACAGCCCCATGTACTTTTCTCA
 GTCATTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCAACCCCTAAAATGTTGGA
 CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTCTTCTTCAT
 TGCTCTTGTCCATGTGGAAATTTTATCTTGTGCTGCGATTGCCTTTGATAGATACACAGTGA
 25 TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC
 TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTGT
 ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
 GGCCTGTGCCGGGACCTTTGTAAGAATATACAATGCTCATACTTGCCGGCATCAACTTC
 ACATATCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
 30 GCGCTCAGCAGAAGGAAGGCAGAAGGCCCTTTCCACATGTGGGTCCCACATCTGACAGCTGT
 CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG
 GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
 TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
 GTTAA (SEQ ID NO: 256)

35

AOLFR139 sequences:

MGFPGIHSWQHWLSLPLALLYLLALSANILILIINKEAALHQPMMYYFLGILAMADIGLATTIMP
 KILAILWFNAKTISLLECFAQMYAIHCFVAMESSTFVCMADRYVAICRPLRYPSIITESFVKAN
 GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS
 40 DLGLILSYALILYSVLKLSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
 HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCCTGGCTCTGCTCT
 ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
 45 GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
 ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
 AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
 CTGCAATGGCTATTGATAGATATGTAGCCATTTGTGCGACCGCTACGATATCCATCAATCATC
 ACTGAATCTTTTGTTTTCAAAGCAAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
 50 TCTCAGTGCTCTGTTGGCTGCCAGAGGCATTACTGCTCCCAGAAATCAAATTGAGCACTG
 TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
 AACCAGGTCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTATCAT
 ATGCTCTAATACTTTACTCTGTCTGAAGCTGAAGTCTCCAGAAGCTGCATCCAAGGCCTT
 AAGTACCTGCACCTCCCACCTCATCTTAATCCTTTTCTTCTACACAGTCACTATTGTGATTT
 55 CCATTACTCGTAGTACAGGAATGAGAGTCCCCCTTATTCCAGTTCTACTTAATGTGCTACA

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
 GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
 TCTATTTGGAGTGTCTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA
 TCTTAATCCGAAGTATTCCCACTTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT
 5 TTTTGGATTCTGGTATACCTCTGTGTATACCCCAAAATCCTGGCCAGTTGTGTCTCAGA
 AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTCTGTGTGTAGCCT
 ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
 ATTGCTTTATTACAGGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGTGTGGCTCCTACA
 TAGGAGGATTTTTGAATGCCATAGCCATACTGCCAATACATTCCGCTGCATTTTGTGG
 10 TAAAAATATCATTGACCACTTTTTCTGTGATGCACCACCATTTGGTAAAAATGTCTGTACA
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA
 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGACAAA
 15 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCTCTCATCTATAGCCTGAG
 AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
 A (SEQ ID NO: 250)

AOLFR136 sequences:

20 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVTVVGNLGMILLIAVSPLLHTPMYYFL
 SLSFVDFCYSSVITPKMLVNFLGKKNITLYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
 SPLLYNAIMSSWVCSLLVLAFFLGLFSLALHTSMMKLSFCKSHIINHIFCDVLPLLNLSCSNT
 HLNELLFIHAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSHLMVVIFFGSITFMY
 FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

25
 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG
 CAGAGCTCCAGCTGCCCCCTCTCCTCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG
 CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
 30 TCCTCAGCAGCTTGTCTTCGTCGATTTCTGCTATTCCTCTGTCACTACTCCAAAATGCTG
 GTGAACCTCCTAGGAAAGAAGAATACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
 TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
 TGTGTCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC
 TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCTTGAATGAGTGCATGATGATGATG
 35 AAATGTCCTTTTGCAAATCCCAATTATCAACCATTACTTCTGTGATGTTCTTCCCCTCCT
 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTTA
 ACACCTTGGTGCCCACTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
 CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGAACATGCAGCTCTCATCTCATGG
 CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTCAAGCCCCCTTCAAGTAACTCC
 CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT
 40 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
 AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

45 MSPENQSSVSEFLLGLPIRPEQQA VFFALFLGMYLTTVLGNLLIMLLIQLDShLHTPMYFFLSH
 LALTDISFSSVTVPKMLMNMQTQHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL
 HYATIMTQSQCVMLVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGAALLKLSGSDTSL
 NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTHIGLYFLP
 PSSNTNDKNILASVIYTA VTPMLNPFIYSLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ
 ID NO: 253)

50
 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCTCCTCCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTCTGCGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
 TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 55 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT
 TTTTCATATTTTTGCTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT

WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFILIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

5 ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTGTACACAGCAATTGTGCTGGGGAATTCCTCATTGTGCTCACTGTC
ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCCAAACATCATCTCAGATCTGCTGGCTGAAAGGAAA
10 GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA
GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC
TACACCACCATCATGAACTGGCAGGTGTGTAAGTGTGCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTGCCTGCTCTGACACCT
15 TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTGGGGT
CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCCTGGAGCTCTGAAGGGTGG
TGCAAGCCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCTGTCTACTCTCTGAGAAATGCTGAAATGAG
20 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
NO: 246)

AOLFR134 sequences:

MTTILEVDNHTVTTRFILLGFTRPAFQLLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
25 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSC
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS
S (SEQ ID NO: 247)

30 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC
AGCCCCAAGATGCTTGTGACTTCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
35 TGACTCAACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAAC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTATAGCAAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
40 CTCTTGCCCTCATGGTCATTGCTATTCCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCCCTCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTACCTATGCCCGTC
CCAAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT
CCAATCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
45 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
50 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPILLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIIDHFFC
DAPPLVKMSCTNTRVYEKVLGVLGVTLSLAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPP
T (SEQ ID NO: 249)

55

CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC
ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

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AOLFR131 sequences:

MASTSNVTELIPTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIIQILVIIQLPFCGPNVIDHYFCDLQPLFLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLNRNHSAGRHKALSTCASHITVVILFFGPAIFLYMRPSSTFTED
KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

10

ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGTATGCTTTGTGGTGTCTCTCCCGTGTACCTTGCCACGGTGGTGGGCAATGG
CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCTTA
GCTGCCTGTCCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCCATAATTCATCATAGAC
TTACTTGCCAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAATTGAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCTCATCTTGGTGTCTCTTATATTGTCATTCTGGTCAACTTGAGGAACCAT
TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTCACTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

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AOLFR132 sequences:

MVATNNVTEIIFVGFQSNWSEQRVISVMFLLMYTAVVLGNGLIVVTLASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL
HYMAIMNQRMCGLLVRIA WGGGLLHSVGQTFILFQLPFCGPNIMDHYFCDVHPVLELACADT
FFISLLIITNGGSISVVSFFVLMASYLILHFLRSHNLEGQHKALSTCASHVTVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVITYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

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ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTGTCATGGCCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
AGGATAGCATGGGGCGGGGGCTGTGCACTTCTGTTGGGCAAACCTTCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCCTGCACCTCCTGAGAAG
CCACAACCTTGGAGGGGCAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC
GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

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AOLFR133 sequences:

MTEFIFLVLSNPQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN

55

GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT
 TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCA
 TGAAGTCCTTATATTACAGATTAACCTTCTGCAATTCTAACATAATACATCATTTTTACTGTG
 ATATTATAACCACTGTTTATGATTTCTGTACTGACCCTTCTATTAATTTTCTAATGGTTTTTA
 5 TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTTCTACACATTTGCT
 CTTTTCACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
 GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT
 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC
 CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAACAAGTAATAGATTCATTACAAA
 10 AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

METQNLTVVTEFILLGLTQSQDAQLLVFVLVLFYLIILPGNFLIIFTIKSDPGLTAPLYFFLGNLA
 LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMFAFDRIYAICRPLHY
 15 STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
 LMVSNGLLSLLCFLGLLASYAVILCRIEHSSEGKSKAISTCTTHIIIFLMFGPAIFYTCPFQAFP
 ADKVVSFLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
 20 AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
 AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT
 TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCCAGGATGTTG
 GTGGACTTCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
 TCTTGCAATTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC
 25 ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
 TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
 CACTTGCCTTTCTGTGGCCCAAACAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
 CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
 CTCAGCCTCCTGTGCTTCTTGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTCGTATAAG
 30 GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT
 ATATTTCTCATGTTTGGACCTGCTATTTTCTACTACACTTGCCCTTCCAGGCTTTCCAGC
 TGACAAGGTAGTTTCTCTTTCCATACTGTCATCTTCTTGTGATGAACCTGTTATTTATA
 CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
 CTGA (SEQ ID NO: 238)

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AOLFR129 sequences:

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFALFSVI
 YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
 QIFLLHLLGGVEMVLLVSMFAFDRIYAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
 40 AVNLPFCGPNVDSIFCDLPLVTKLACIDIYFVQVIVANSGLSLSCFIILLISYSLILITIKNHSPT
 GQSKARSTLTAHTVILFFGPCIFIYIWPFGNHSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK
 KLWRAFVNSREDT (SEQ ID NO: 239)

ATGGCTCTTTATTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTCTACAGG
 45 TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAAATCAATCTCAAGTGTC
 AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTCTTTGCCCTCT
 TCTCGGTATCTATGTGGTCACAGTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAAC
 ACCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTTGTAGATATGAC
 CCTTGTCTCTTTTGCCACCCCTAAGGTGATTCTGAACTTGTTAAAAAAGCAGAAGGTAATT
 50 TCTTTTGTCTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
 ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCCTACACTACATG
 ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC
 TTCCTCAGGGTTTTCAGATACCATTGCTGTGAACTTGCCCTTTTGTGGTCCCAATGTGGTA
 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCCTGTATAGACATATATTTGT
 55 ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTGCTTA
 TCTCCTACAGTCTGATCCTCATAACCATTAAGAACCCTCTCCTACTGGGCAATCTAAAGC

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCG
ACATTTGTCTTCTTAGACCTGTGTCTCATTCTGCCACAGTCCCCAAATCCATCCTCAACT
5 CTGTCGCCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
TCTGCTGCCCCCTACACTGTGAGGCTGTGATGAGCAGAGGGGCTCTGTGTCCAGTTGATGGC
TCTGTCCTGGCTCAACAGAGGGGGCCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG
AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
10 CACTTGTCTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
TTTTCATGTTTAGTTTGCATTGTAGTTTCTATGTGTACATTTTCTCTGCTGTGTTAAGGAT
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATTGTTGTC
ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT
15 ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

MFLYLCFIFQRTCSEEMEEENATLLTEFVLGTGLHQPDCIPLFLAFLVYILITIMGNLGLIVLIW
20 KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSRLTFCNSNIIHFYCDII
PLLKISCTDSSINFLMVIFAGSVQVFTIGTILISYTHLFTILEKKSIGIRKAVSTCGAHLSSVSLY
YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
NO: 233)

25 ATGTTCTTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTACATCAACCTGACTGTAAAAT
ACCGCTCTTCTGGCATTTCTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
30 TTGTTCTCATCTGGAAAGACCCCTCACCTTCATATCCCAATGTACTTATTCTTGGGAGTTTA
GCCTTTGTGGATGCTTCGTTATCATCCACAGTACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAAACCCT
GTAACCACAGAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTCAGCTATTAGTCTTGCA
TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTCATTGAGTTAACCTTCTG
35 TAATTCACATAATAACAACACTTTTACTGTGACATTATCCCATTTGTTAAAGATTTCTGTA
CTGATTCTCTATTAACCTTTCTAATGGTTTTTATTTTCGCAGGTTCTGTTCAAGTTTTTACCA
TTGGAACATTTCTATATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
40 GATGGAGTCTCTATTTTACACTGTCTAGTTCTTTTATTAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID
NO: 234)

AOLFR127 sequences:

45 MSNEDMEQDNTLLTEFVLGTLYQPEWKMPFLVFLVYILITTVWNLGLIALIWNQPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHFYCDIPLFMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLSSVSLYYGPLIF
MYLRPASQPQADDQDMIDSVFYTHIPLNPIIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)

50 ATGTCGAATGAGGACATGGAACAGGATAATAACAACATTGCTGACAGAGTTTGTCTCACA
GGACTTACATATCAGCCAGAGTGGAATAATGCCCTGTTCTTGGTGTCTTGGTGATCTATC
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTTAC
ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
55 AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTCTTTGCATTTGGTGGAACTACAGAATGTTTTCTTGGCAACAAT

MMLPFCGNNVIDHITCEILALLKLVCSDITINVLIMTVTNIVSLVILLLLIFISYVFILSSILRINCAE
GRKKAFSTCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

5 ATGTACAGATTTACAGATTTTGTATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
GACTGAATTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCCTGC
TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
10 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT
CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTGTGTGCCCTTGGCTTGGGCTCCACTGAGTGT
GTCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
CCATCATCATGAACGGAGTGCTGTATGTGCAAAATGGCTGCATGGTCTGGATCATAGGCTG
TCTGACCTCCCTATTGCAAACAGTTCTGACAAATGATGTTGCCTTTCTGTGGGAATAATGTC
15 ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTTCAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
TTTTATGTACATGAAACCCAAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG
20 TCTTATGGAGTGGTAAGCCCAATGTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTATTGAAAATGTGA (SEQ
ID NO: 228)

AOLFR124 sequences:

25 MNHSVVTETFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIIAKIYNNLTHTPMYVFLTLAVV
DICTTSIIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST
VMNHHMVCVALLSMVMAIAVNTSWVHTALIMRLTFCGPNTIDHFFCEIPPLLALSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVEGKRKAFSTCSSHLTVVTLYYSPVIYTYIRPASS
YTFERDKVVAALYTLVTPTLNPVMVYSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)

30 ATGAATCACAGCGTTGTAACCTGAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACCTCC
AGGGAATTATCTTCCTCTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTGCCAAAATCTATAACAACACCTTGCATACGCCCATGTATGTTTTCTTCTGAC
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
35 GCTAACATCAGAAAATACCATTTCATATGCAGGCTGCATGTCCAGCTCTTCTTGTTCACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTTCCTCTTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATAACCCCATGCTGGCTTTG
40 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAACCCGATGGTG
45 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

50 MTNQQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKLSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICPLHC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSEKHA
ISVSVAIGVCYAFSCLVCIVVSYYVYFSAVLRISQRQRQSKAFSNCVPHLIVVTVFLVTGAVAYL
KPGSDAPSILDLLSVFYFVAPPTLNPVTYCLKNKDIKSALSKVLWNVRSSGVMKDD (SEQ ID
NO: 231)

55

GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

AOLFR121 sequences:

5 MKRKNFTEVSEFIFLGSSFGKHQITLFVVFLTVYILTLVANIIVTIIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMVHLVTAMFNLPFCGTVVDHFFCDIYPVMKLSCIDTTINEII
NYGVSSVFIVPIGLIFISYVLVISSILQIASAEGRRKTFATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVTYTIITPLLNPVVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

10 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTAACTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCAATTGTGCCACGAATGCTT
15 TTGAGCCTCATTTTTTATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
TTTTGTTATCTTGGCCACTAATAATTGCTTCTGCTTACTGCAATGGGGTATGACCGCTATG
TGGCCATCTGCAGACCCCTGAGATACACTGTCTCATGAGCAAGGGACTATGTGCCAGCT
GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT
AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTGTGACATTTACCCAGTCATGA
20 AACTTTCTTGCATTGATACCCTATCAATGAGATAATAAAATTATGGTGTAAGTTCATTTGT
GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCTTGTCTCTCCACCTCATCTT
AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
ATAGAAAAAGACCTTGTTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCCTG
25 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

30 MEWENQTLVEFFLKGHSVHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSTIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN
EFLMLVATILFTLMPLLLVISYSLIISILKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDL DATDKIISMFGVMTMPMNPLIYSLRNKD VKEAVKHLPNRRFFSK (SEQ ID NO:
225)

35 ATGGAATGGGAAAACCAAACCATTTCTGGTGGAATTTTTTCTGAAGGGACATTCTGTTCAACC
CAAGGCTTGAGTTACTCTTTTTGTGCTAATCTTCATAATGTATGTGGTCACTCTTCTGGGG
AATGGTACTCTCATTTTAAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
40 TGAGCTTCCTTTCAGAAAGAAAGACCATTTCTTTTCTGGCTGTGCAGTGCAGATGTTCTT
GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
TGGCTATCTGCAACCCTCTGAGATATCCCATCATGAGCAAGAATGCCTATGTACCCAT
GGCTGTTGGGTCCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA
CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCAT
45 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
TTCACATTGATGCCACTGCTCTTGATAGTTATCTCTTACTCATTAAATCATTTCCAGCATCCT
CAAGATTCACCTCTGAGGGGAGAAAGCAAAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
CACTTAATTCAGATGACTTGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
50 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

55 MYRFTDFDVSNISIYLNHVLFTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
IMYMIILLGNSLLIITILDSRLHTPMYFFLGNL SFLDICYTSSSIPPMLIIFMSERKSISFIGALQM
VVSGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLLQTVLT

TTGCCAGTTGGTTCTGGCATGGCTTGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
 TATATTTTGATTCTGTACTCTGTACTTAGACTGAAGCTGAGCTGAAGCTGCAGCCAAGGCC
 TGAGCACTTGTAGTTCACATCTCACCCTCATCTTTTCTTTTACACTATTGTTGTAGTGATT
 TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
 5 ACAACATCATCCCCCTTCCCTCAACCTACAGTTTATGCACTTCAGACCAAAGAAGCTTAG
 GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
 218)

AOLFR119 sequences:

10 MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
 MYFFFGHALSLIDLLTCTTTLPNALCIFWFSLEINFNACLAQMFFVHGFTGVESGVLMLMALD
 RYIAICYPLRYATTLTNPIIAKAEATFLRGVLLMIPFPLVKRLPFCQSNIIISHTYCDHMSVVKL
 SCASIKVNVIIYGLMVALLIGVFDICISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIHITYVPA
 FFTFFAHRFGGHTIPPSLHIIVANLYLLPPTLNPIVYGKTKQIRKSVIKFFQGDKGAG (SEQ ID
 15 NO: 219)

ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
 TCTTAATGGAATACCTGGTCTGGAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
 ATGTACATCATCTTCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTATTATGAGGAGTC
 20 CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
 CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
 ATGCTTGCTTGGCCAGATGTTCTTTGTTTCATGGGTTTACAGGTGTGGAGTCTGGGGTGCT
 CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC
 TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGTATTGCTGAT
 25 GATTCTTTTCCCATCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCATA
 CGTACTGCGACCAACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
 CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTTGACATTTGTTGTATATCTTTGCTT
 ACACCTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
 CAGCACCTGCACTGCCATATATCTGCCATCATCATCCTATGTTCCAGCATTCTTCACTT
 30 TCTTTGCCACCGTTTTGGGGGACACACAATCCCCCTTCTCTTACATCATTGTGGCTAAT
 CTTTATCTTCTTCTTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
 ACGCAAGAGTGTCAAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

AOLFR120 sequences:

35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMLFTLVENLAAILVVGLDHRLRRPMYF
 FLTHLSCLEIWTYSVTVPKMLAGFIGVDGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
 VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPIYLLSQLTCGPNVIDHFSCDASPLLALS
 CSDVTWKETVDFLVSLAVLLASSMVIAVSYGNIVWTLHRSAAERWKAFSTCAAHLTVVSLF
 YGTLFFMYVQTKVTSSINFNKVVSFYSVVTPLNPLIYSLRNKEVKGALGRVFSLNFWKGGQ
 40 (SEQ ID NO: 221)

ATGCAACCATATACCAAAAAGTGGACCCAGGTAAGTGAATTTGTCATGATGGGCTTTGCTG
 GCATCCATGAAGCACACCTCCTCTTCTTCACTCTTCCCTCACCATGTACCTGTTACCTTG
 GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
 45 ATTTCTTCTGACACACTTGTCCTGCCTTGAATCTGGTACACTTCTGTTACAGTGCCCAAG
 ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT
 CCCAGCTCTTCATCTTCACTTTCTTGGGGCAACTGAGTGTTTCTACTGGCTGCCATGGCC
 TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGCTGCTGGGGCAC
 CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCTCACCACCATCTTGCCAATCT
 50 ACCTCTGTCTCAGCTAACATTTTGTGGCCCAAATGTCAATTGACCATTTCTCCTGTGATGCC
 TCACCCTTGCTAGCCTTGTCGTGCTCAGATGTCACTTGAAGGAGACTGTGGATTCTCCTGG
 TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCAATTGCTGTGTCTATGGCAACATCGTC
 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCCTTCTCTACCTGTGCAG
 CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTCTTTATGTATGTCCAGACCAAG
 55 GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCCAT

GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCTGGATTATAGGTATTATCACTCAGTGATTCAAGTTGGCTTTTGTGTA
GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTTAT
CAAACCTGGCTTGCATAGAGACCTACACATTGGGATTTCATGGTTACTGCCAATAGTGGATTT
5 ATTTCTCTGGCTTCTTTTTTAATTCCTCAATAATCTCTTACATCTTTATTTTGGTGACTGTTTCAG
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG
TGGTTTTGGTCTTTGGGCCATTAATCTTTTTCTATATTTTCCATTTCCACATCACATCTTG
ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
10 AGTAAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLLIYVTSIMGNSGIILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT
15 EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHFFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSEMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

20 ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCCTTCTCTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTTCTATC
TTCTGGGATTTGGTGCCAGCATGAGTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC
TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT
25 TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
30 TGTACAAACAGGTTTTACATGTTCACTGTCTTCTGCAAGTCCAATGTTGACATCAACATCATGCTA
CTTGTGTCTTTGTGGGATCTAACTTGATATTCACTGGGTTGGTTCGTCATCTTTTCTACAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAATCCTTCTCA
ACATGTGCTTCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
35 GCAGTCTCATTTCTAATAATTCCCAGGAAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

AOLFR118 sequences:

40 MNHMSASLKSNSKQVSEFILLGFPGIHSWQHWSLPLALLYLSALAANTLILIIWQNPSLQQ
PMYIFLGILCMVDMGLATTIIPKILAIWFDAKVISLPECFAQIYAIHFFVGMESGILLCMAFDRY
VAICHPLRYPSTVSSLLKATLFMVLRLNGLFVTPVPVLAQRDYCSKNEIEHCLCSNLGVTS
CDDRRPNSICQLVLAWLGMGSDLSLILSYILILSVLRNLNSAEAAAKALSTCSSHLTLILFFYTIV
45 VVISVTHLTEMKATLIPVLLNVLHNIIPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCTGGCA
CTACTGTATCTCTCAGCACTTGCTGCAACACCCTCATCCTCATCATCTGGCAGAACCC
50 TTCTTTACAGCAGCCCATGTATATTTCCCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGATGGCTTTTGTAGATATGTGGCTATTTGTACCCTCTTCGCTATCCATCAATTG
TCACCAGTTCCTTAATCTTAAAGCTACCCTGTTTCATGGTGTGAGAAATGGCTTATTTGTC
55 ACTCCAGTGCCTGTGCTTGACGACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT

ATGGAAAGAATCAACCACACCAAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
GGCCTGAGGACCAAAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC
AGGGAACCTGCTCATCATCCTGGCCATTGCGTTCAACCCCATCTTCAAGACCCCTATGTATT
TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCAAGATG
5 CTGATGAACTTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
CTATGTGGCCGTCTGTGACCCCTTCCACTATGTCAACCACCATGAGCCACCACCACTGTGTCC
TGCTGGTGGCCTTCTCCTGCTCATTTCCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCACCTTCTCTGTGACCTCAGCCCTGT
10 GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTTATATACGAATCCTCACTACAGT
TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTTCATCCATGCTCAATCCTT
15 TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

MEGFYLRRSHLEQMGKPGRVNQTTVSDFLLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLII
20 LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTMSPLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMITMGLLFLTVPPLLIVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLRNRDMKEALG
KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
30 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
CCTGTCAATTAAGTATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACAGCTATATTTCCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT
GTGCTGGGTGCTAACCACCTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
35 TTCTGTGCCCCAGAAAGCCATCGCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCCTACT
GTTCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTCTCTC
ATCTCCTGGAGGGAGATGGAAGGCCTTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTTACTCTACAGAGAG
40 GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTTCCACGCTAAACCCATTCAATTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTCTAGTGAAAAACA
TTCTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLAN
45 LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCILFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
TANSGFISLASFLIISIYIFILVTVQKKSSGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPFTSHLD
KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTTCTCTTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCT
GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTCTCCACAGCTCCCAAGATGATT
55 ATGACCTTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGGAACCTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT

SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPIIYSLRNKAIKVALGMLIKG
KLTKK (SEQ ID NO: 205)

5 ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
TTTCCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
TGGGGTTTTCTACCAATAAAAAATATGTGCATTTTGCATTTCGATTCTCTTCTTGTGATTTAT
TTGTGTGCCCTGATGGGGAATGTCTCATTATCATGATCACAACTTTGGACCATCATCTCC
ACACCCCCGTGTATTTCTTCTTGAAGAATCTATCTTCTTGGATCTCTGCCTTATTTCAAGTC
ACGGCTCCCAAATCTATCGCCAATTCCTTGATACACAACAACCTCCATTTCAATCCTTGGCTG
10 TGTTTCCAGGTCTTTTGTGCTTCTTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
TGTCTTTGACCGCTATACTGCTATATGTACCCCTCTGCACTATGATGTCATCATGGACAGG
AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT
GACATTCCCCAGTTATTAGCTATTTCTTGTCTCAGAAAATTTAATAAGAGAAAATTGCACTCA
15 TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
GCCTTCCACACTTGTGCTGGTTGTGTTATTTCTTCCACTGGATTCAATTGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
20 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

15 MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSQSSDWMQLCTHLCTLSVFFPSWSCGIQLPLSLRCCLIFSVRRKPFLLQDASFRPTSS
TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFIILITFFIMISYARIIGAVLKIKTASGRKK
AFSTCASHLAVVLIFGSIIFMYVRLKKSYSLTLDRTLAIVYSVLTMPMVNPIIYSLRNKEIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

30 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTGTGTCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTCTGTGTTCTGGCTGCTGTGGACATTGTTA
35 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
40 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCTTGCACACCCAAGTCCTGC
45 TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
CTGGGTTTCATGA (SEQ ID NO: 208)

AOLFR114 sequences:

50 MERINHNTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTTGNLLIILAIRFNPHLQTPMYFFLSFLS
LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF
HYVTTMSHHHCVLLVAFSCSFPHLHSLHTLLNRLTFCDNSNVIHHFLCDLSPVLKLSCSSIFVN
EIVQMTEAPIVLVTRFLCIAFSYIRILTTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP
PSTYAVKDHVATIVYTVLSSMLNPFYIYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

AOLFR109 sequences:

MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
 HLSLLDVCFTTTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGAECILLAFMAYDRYVAICY
 5 PLNYVPISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 PHSTHGPDKDKPFSLLYTHTPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
 201)

10 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTCAGCAGAGCTCCA
 CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTGGCCCTCTACAGCCTCACCATGGCCATG
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTTCTCGGCCATCTGTCTCTGCTGGATGTCTGCTTCATCACCCTACCATCCACAGATG
 TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
 15 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGATCCTCTTGGCTTTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAAGTATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
 GGCTTGTGGGAACCTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTT
 ATTCCGAGAGCCCTTCCGCAGAGACAACACATAGAAAAGCTTCTTGTGAGGCCCCCATA
 GTGATTGGCCTCTCTTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
 20 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCTTATGTGCACATCCTGGCCACC
 ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
 TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCATGTGCA
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
 25 GAAGAACCAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
 DASYSFVAPRMLVDLSEKKVISYRGCTQLFHLHFLGGGEGLLLVVMAFDRIAICRPLHCST
 30 VMNPRACYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL
 LMVFNGLMTLLCFLGLLASYA VILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFYMCPF
 RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
 203)

35 ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCTCCCTGGA
 AATTTTCTCATTATTTTACCATAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT
 TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTTGG
 TGGACTTCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
 40 CTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCTC
 CGCTTGCTTTTTGTGGCCCAAACACAGCTGGACAACTTCTTCTGTGATGTCCGACAGGTCA
 TCAAGCTGGCTTGACCCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
 45 GATGACACTCCTGTGCTTTCTGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTT
 GTAGGCGAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCATTA
 TTATACTTCTTATGTTTGGACCTGCTATCTTCATCTACATGTGCCCTTTTACGGGCCTTACCA
 GCTGACAAGATGGTTTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
 TACCTTCGCAACCAGGAAGTGAACAACTTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
 50 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTVTEFILMGFSTNKNMCIILHSILFLLIYLCALM
 GNVLIIMITTLDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQVFLLLSS
 55 ASAEILLLTVMSEFDRTAICHPLHYDVIMDRSTCVQRATVSWLYGGGLIAMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCSNLIIEIALILINVLDFFCFIVIIITYVHVSTVKKIPSTEGQSKAY

GAAACTTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT
 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT
 TTCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCTTTACGTAATCCCATT
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA
 5 TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSFILVILNDSGSPPELLCATITILYLLALISNGLLLLITMEARLHMPMYLLLGQ
 LSLMDLLFTSVVTPKALADFLRRENTISFGGICALQMFLALTMGGAEDLLAFMAYDRYVAICH
 10 PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYHPCRAQEIRHLLCEIPHLLKVACAD
 TSYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGA
 ATFMVYLPSSFHSTRQDNISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL
 (SEQ ID NO: 197)

15 ATGGAGCTCTGGAACCTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC
 CTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACTCCCAAGGCCCT
 TGCGGACTTTCTGCGCAGAGAAAAACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT
 20 CTGGCACTGACAATGGGTGGTGTGCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
 ATGTGGCCATTTGTATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCCTGGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC
 ATGCACTATCCCTTCTGCAGGGGCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 25 GACCTTCTGATTCCCTCTCTGTGCTGCTATACTGGCCTCCTATACACAAATTCTACTCACTG
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTTCATGTATGTCTTGCCAGTTCCCTTCC
 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCTATGCGGGCCTTGAGGAGGGTCTCTGGG
 30 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFIYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLLVGTECALLAV
 35 MSYDRYVAVCKPLYYSTIMTQVRVCLWLSFRSWASGALVSLVDTSFTFHLPHYWGQNIINHYFCE
 PPALLKLASIDTYSMAIFSMGVVILLAPVSLILGSYWNIISTVIQMOSGEGRLKAFSTCGSHLI
 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTAVTPMLNPIIYSLRNKDVKGALRKLVRKC
 FSHRQ (SEQ ID NO: 199)

40 ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGACAGACCCAGAT
 CCTGCTATTTATCCTTTTCTCATCATTTATCTGCTGACCGTGCTTGGAACCAGCTCATCA
 TCATTCTCATCTTCTGATTCTCGCCTTACACTCCCATGTATTTTTTTCTTAGAAATCTCT
 CTTTGCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCACTTCTTGGTA
 45 AAGAGGAAAACCATTTCTTTTATGGGTGTATGACACAGATAATTGTCTTCTTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA
 GCCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCCAGGCTCT
 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATAACAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 50 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC
 CTGCTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCTCTCT
 CTATGGGTGAGGAATATTCACCTACATGCGACCAAACTCCAAGACTACAAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
 55 TTGAGGAACAAAGATGTCAAAGGGCTCTCAGGAAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR105 sequences:

25 ATGCAGGGGCTAAACCACACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC
CCACCTCCAGCTGATGCTCTTCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA
ACCTGTCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
30 CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTGTCCTGTGCCAGTCAGATGTTCTT
CTCCTTCAGCTTCGGCTTCACCCACTCCTTCTGCTCACTGTCATGGGCTACGACCGCTACG
TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC
35 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTTCTTCTGCCACGTGCCACCTCTGTT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTGGTGTGTAT
CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCTCTCTATGCCTTCATCGTGGCCGCCA
TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
CACTGTGGTGGTTCGTGCACATATGGCTTGCCTCCGTCATTTACCTGAAGCCCAAAGGTCCC
40 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCTCACACCCTTCTCA
GCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
CACCAAACCTCTTCCACAGAAGTGTGA (SEQ ID NO: 194)

AOLFR106 sequences:

40 METANYTKVTEFVL TGLSQTPEVQLVLFVIFLSFYLFILPGNIIICTISLDPHLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIISFDGCI AQLFFLHFAGASEMFLLTVM AFDLYTAICRPLHYA
TIMNQRLCCILVLRCSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCLIALLSYAFLLALFKKLSGSGENTN RAMSTCYSHITIVVLMFGPSIYIYARPF
SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVT KYILCKEK (SEQ ID NO: 195)

45 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
CAGAGGTCCAAGTAGTCTATTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
AATATCCTTATCATTTGCACCATCAGTCTAGACCCCTCATCTGACCTCTCCTATGTATTTCT
50 GTTGGCTAATCTGGCCTTCCTTGATAATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCT
CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGCATGGCCTTGACCTCTACA
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
GTGGCTCTCTCCTGGAGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTGTTCT
GACTTCTTTCTGTGGGCCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT
55 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
ATCTCTGTGGTGTGTTTGATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGTTCAA

LVDFVINSCKILATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
KSYSLDYDQALAVVYSVLTPLNPFIFYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

5 ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCATCTCC
AGGGTGTCCAGATTTATCTCTTCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
TTGTCAGCATTCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
GCAAACCTTGCTCAGTGAGAAAAAGACCATTTTATTCTCTGGGTGTCTCCTGCAGATCTATT
TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
10 TTTAGCCATCTGCCGGCCCCCTCCACTACCCAACCTCATGACCCCAACACTTTGTGCAGAG
ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGATTT
CACGCCTCCCATTCTGTGGCCCCAATCGCATTTCAGCACGTCCTTTGTGACTTCCCTCCTGTG
CTGAGTTTGGCTTGCAGTACGCTCTATAAATGTCCTAGTAGATTTTGTATAAAATTCCTG
CAAGATCCTAGCCACCTTCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
15 TCAGAATTCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCCTTCTCAACC
CCTTCATCTACAGCTTGCAGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

20

AOLFR102 sequences:

MPVGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIWVVCSTHSLRTPMYF
FLSNLSFLELCYTTVVVPLMLSNIILGAQKPISLAGCGAQMFFVTLGSTDCLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVRLACA
25 DIRVHQAVLYVVSILVLTIPFLICVSYVFITCAILSIRSAEGRRRAFSTCSFHLTVVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLLNPLLYSLRNKDVKGALRSAIRKAASDAN (SEQ ID
NO: 189)

30 ATGCCTGTGGGGAAACTTGTCTTCAACCAGTCTGAGCCCACTGAGTTTGTGTTCCGTGCGT
TCACCACAGCCACTGAATTCCAGGTTCTTCTCTTCTTCTTCTCCTCCTCTACTTGATG
ATCCTCTGTGGCAACACAGCCATCATCTGGGTGGTGTGCACACACAGCACCCCTCCGCACCC
CGATGTATTTCTTCTGTCCAACCTGTCTTCTTCTGGAACCTCTGCTACACCACCGTGGTAGTA
CCCTTGATGCTTTCCAACATTTTGGGGGCCAGAAAGCCCATTTCTGTTGGCTGGATGTGGGG
CCCAAAATGTTCTTCTTTGTCAACCTCGGCAGCACGGAAGTTCCTCTTGGCGATCATGGCC
35 TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACACCCTCATCATGACCCGCGAGC
TGTGCACGCAGATGCTGGGTGGGGCCCTGGCCCTGCGCCCTCTTCCCCTCCCTGCAGCTCAC
CGCCTTAATCTTCAACCTGCCCTTTTGCAGGCCACCAAGGAAATCAACCACCTTCTCTCGC
ATGTGCCTCCCGTCTGCGCTGGCCTGCGCTGACATCCGCGTGCACCAAGGCTGTCCTCTA
TGTCGTGAGCATCCTCGTGCTGACCATCCCTTCTGCTCATCTGCGTCTCCTACGTGTTCA
40 TCACCTGTGCCATCCTGAGCATCCGTTCTGCCAGGGGCCCGCCGGGCTTCTCCACCTG
CTCCTTCCACCTCACCGTGGTCTGCTGCAGTATGGCTGCTGCAGCCTCGTGACCTGCGTC
CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCGTTGGTCTACACCTTTGTAC
CCCCTTACTCAACCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG
AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCAACTGA (SEQ ID NO: 190)

45

AOLFR103 sequences:

MAEMNLTIVTEFLIAFTEYPEWALPLFLLLLFMYLITVLGNLEMIIILMDHQLHAPMYFLLSH
LAFMDVCYSSITVPQMLAVLLEHGAALSYTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ
PLLYVTILTQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLKLTGCEST
50 QEVLIIMFAIFVIPASMVVILVSYLFIIVAIMGIPAGSQAFTSTCTSHLTA VSLFFGTLIFMYLRG
NSDQSSEKNRVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

55 ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCTCTTGTATTATTATGTATCTCATCACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCT
TCTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCCAGATGCTGG

TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
TCTACACAGTGGTGATCCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

5 **AOLFR98 sequences:**

MRGFNKTTVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEI
LSFSESCYTFVVIQQLVHLLSDTKISFMACATQLFFFLGFACTNCLLIAMGYDRYVAICHPLR
YTLIINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE
10 LALFSLVIMVFPFLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVFVHYGCASIYLRPKSK
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTGTGTCATCTTCTCTCTACTTGACAATCCTGGTG
GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCAACTCCCATGTATG
15 GCTTTCTATTATCCTTTTCTGAGTCTGCTACACTTTTGTGTCATCATCCCTCAGCTGC
TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
CTTTTCTCTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
ATGTAGCAATTTGTACCCCTCTGAGGTACACACTCATCATAAACAAGGCTGGGGTTGGA
GTTGATTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
20 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCACTATTTCTGTGACATGGCACCTGT
TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTAGCCTCAGCATC
CTGGTAATTATGGTGCCTTTTCTGTTAATTCATATCCTATGGCTTCATAGTTAACACCAT
CCTGAAGATCCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTCACCTGTGCCTCACATCTCACT
GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
25 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
CTTGCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTCTTGAATG
CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

AOLFR99 sequences:

30 MERVNETVVRVIFLGFSSLARLQQLFVIFLLLYLFTLTGNAMISTIVLDRALHIPMYFFLAILSC
SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNHFSQIV
IFMLCTLVLAIPLLLILVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

35 ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC
AATGCAATCATCATTTCCACCATTGTCCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
CCTTGCCATCCTCTCTGCTCTGAGATTGCTACACCTTCATCATTGTACCCAAGATGCTGG
40 TTGACCTGCTGTCCCAGAAGAAGACCATTCTTTCTCCTGGGCTGTGCCATCCAAATGTTTTCC
TTCCTCTTCTTGGCTGCTETCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA
CCTGCCITTTTATTCCCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA
45 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
CTGGCTATCCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA
GTTTCTTCCACACTGGGTAGGTGCAAAGCCTTTTCTACCTGTGTATCTCACCTCATTATTG
TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAATACTCCTCA
AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
50 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT
TTCCCTGTTGTAA (SEQ ID NO: 186)

AOLFR101 sequences:

MDTGNWSQVAEFILGFPHLQGVQIYFLLLLLLIYMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
55 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
HYPTLMTPTLCAEIAIGCWLGLAGPVVEISLISRLPFCGPNRIQHVFCDFPPVLSLACTDTSINV

TCGCCCCACTTCAGAGACTGTCTTGTTCTGATCTCTTTATCCATAGAATGATATCTTTTTCT
 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
 TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
 CTCACCTGGGAGTTGTGAGTGTGCTATGGTGCTGTCTTTTTTATGTATCTCACTCCTGAC
 5 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
 ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAAATTTCTAGA
 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

10 MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAITYTVTLGNFLIVTVTSVDLALQTPMYFFLQN
 LSLLEVCFITLVMVPKMLVDLVSFRKIIISFVCGGTQMYFFFFFGSSECFLLSMMAFYDRFVAICNP
 LHYSVIMNRSCLLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFFCDGPPVLKLVTV
 DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL
 TYLRPKSNQSPESKKLVLSYTVITPMLNPIIYGLRNNNEVKGAVKRTITQKVLQKLDVF (SEQ
 15 ID NO: 179)

ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
 CCGAGATGCAAGTTTCCCTCTTTATTTTTCTGGCCATTTATACAGTCACCTTGTGGGC
 AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
 20 TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTACCTTGGTTATGGTGCCAAAAATGCTTG
 TAGATCTAGTGTCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
 CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTTGT
 GGCCATCTGTAACCCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
 GCCATAGGCTCTTGGATGTCCGGTGTCTCTATGCTACAGACAGCTTGGATGATGG
 25 CCCTTCTTCTGTGGACCAAATGCCGTGGACCACTTTTCTGTGATGGTCCCCCAGTGTTA
 AAAGTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
 TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG
 AGGATGCTCTTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTCTCACACCTCATTGT
 GGTGTCCCTCTTCTACGGAACGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCAAGTCC
 30 CCTGAGAGCAAGAAGCTAGTGTCTGCTTCTGCTACACTGTCATCACACCTATGCTAAACCCCA
 TCATCTACGGCCTGAGGAACAATGAAGTGAAGGGGCTGTCAAGAGGACAATCACTCAAA
 AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

AOLFR97 sequences:

35 MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMFVVPFSIAEHWRMKGANLSQGMFEL
 LGLTDPQLQRLLFVFLGMYTATLLGNLVMFLLIHVSATLHTPMYSLLKSLSFLDFCYSSTVV
 PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC
 ASLIVGSYSAGFLNSLIHTGCFSLKFCGAHVTVTHFFCDGPPLSLSCVDTSCEILLFIFAGFNLLS
 CTLTILISYFLILNTILKMSSAQGRKFAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRVA
 40 VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
 CCTTAGGCAGAATTAAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
 TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
 45 GGAGTTTGAGCTCTTGGGCCTCACCACTGACCCCCAGCTCCAGAGGCTGCTCTTCGTGGTG
 TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG
 TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCTTCTTGGATTTC
 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTTCTTGGCCAAGAGGAAAGTGA
 TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCAGTGAGTGC
 50 TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC
 AACCATCATGTCTCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
 CTAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTCTG
 CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCTTGTCTTGTGTAGACACCTCACTGT
 GTGAGATCCTGCTCTTCTATTTTGTCTGTTTCAACCTTTTGTGCTGCACCTCACCATCTTG
 55 ATCTCCTACTTCTTAATTCTCAACACCATCTTGAAATGAGCTCGGCCAGGGCAGGTTTA
 AGGCATTTTCCACCTGTGCATCCCACCTCACTGCCATCTGCCTCTTCTTGGCACAACTT

GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
 TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
 TGGCTGTCTGTAACCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
 GGTCTTGTGTGCATGGGTGTTTGGGTTTCTTTTCAAATCTGGCCGGTCTATGTCATGTTTC
 5 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
 CAAACTATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG
 TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATCTC
 AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
 TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA
 10 GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACTCCTTTCCTCAATCCTTT
 CATCTTCACCCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
 TGTCAACTATTACAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

15 METWVNQSYTDGFFLLGIFSHSTADLVLFSSVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
 LSQSLMDLMLVCTNVPKMAANFLSGRKSISFVGCIGLQVCLVGEGLLLGLMAYDRYVA
 ISHPLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVMNFPYCGLRKVNHFCEMLSLLKLAC
 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
 AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
 20 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCTTCTCCTCTTAGGCATCTTCTCCC
 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCCGGTCTTCACAGTGGCCCTCTGT
 GGGAAATGTCTCCTCATCTTCTCATCTACATGGACCTCACCTTCACACCCCCATGTACTT
 25 CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
 GCAGCCAACTTCTGTCTGCGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG
 GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGCTGGGACTCATGGCTTATGACCG
 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
 AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
 30 AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
 TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGTCTGTG
 TCTTCATGCTTCTCTTCCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
 GTGCTGCAAATGCACTCTGCTCAGGCCTGGAAAAGGCCCTGGCCACCTGCTCCTCCCACC
 TGACAGCTGTCACCTCTTCTATGGGGCAGCCATGTTCTACCTGAGGCCTAGGCACTA
 35 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC
 ACCCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

AOLFR95 sequences:

40 MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
 GNVGMMTHIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
 LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
 RAVDHFYCDRPLQRLSCSDLFIHRMISFSLSCIHLPTIIVSYMYIVSTVLKIHSTEGHKKAFST
 CSSHLGVVSVLYGAVFFMYLTPDRFPESKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
 45 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGACGG
 CTTACAGGTACGCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTGTGTTTATGCCA
 50 TGATCCTTCTAGGGAATGTTGGGATGATGACCATATTATGACTGATCCTCGGCTGAACAC
 ACCAATGTATTTTCTTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA
 ACCCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG
 GCCCAGCTCTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC
 TTATGACCGCTTTATTGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
 55 TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTGTGGCTGCATTAGCTCAGTTATTAGACT
 AGCATGACATTTACTTTATCTTTTGGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC

SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLLPFIYSLRNEKVQEVLR ETVNRIMTLIQRKT (SEQ ID NO: 169)

5 ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCTGCAAACTCCAATGTACTTCTTCCTCA
GTAATTTGTCCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGGCTGGTTGCATGATCCAAACATATTTCTACT
TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC
10 TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCCTGTCTGTGTTGTTTCCAACCATTGTAAGTGAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTGCCCCCTCTTCTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTCATCCT
GAGCTCCCTGGCATTCACTACTGGGCTCCTACGTGTACATAAATTTCTACCATCCTGCGTATCC
15 CCTCCACCCAGGGCCGTCAGAAAGCTTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC
ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAATCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCCCTTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

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AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRQLQIPMYFFLCNLSFLE
IWYTTTVIPKLLGTFVVARVICMSCCLLQAFFHFFVGTTEFLILTIMSFDRYLTICNPLHHPTIM
TSKLCLQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
25 TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

30 ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCTTGCAGGCAATGGG
CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATCCAATGTACTTCTTCCTTTG
TAACTTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGCAGGCCTTCTTCCACT
TCTTCGTGGGCACCACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCTTTCACCACCCACCATCATGACCAGCAAACTCTGCCTGCAGCTGGCCC
35 TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTTGTGACGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTTGAAG
GCCGCTGCATAGACACCAGCATTTTGGAACCTCTGGGCGTCATAGCAACCATCCTTGTA
TCCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
40 CTCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

45 **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL
SALEILVTTHVPVMLWGLLLPGMQTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTICKSNVNNFFCDRGQLKLSCN
NTLTFEFILFLMAVFVLFGLIPTIVSNA YIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
50 VKPKQTQAADYNWVVSMLMVSVPFPLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

55 ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTGTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA
CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTC
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG

CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWL GASVNSLIHMAILMHF
 PFCGPRKVYHYFCEFAVVKL VCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
 RNAFATCGSHLT VVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
 KALRRVLRD VITQCIQRLQLWLPRV (SEQ ID NO: 165)

5

ATGCTGGACCCAGTATTTCCAGTCACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
 GCTCTTCGATGACTCCCTTACCCACCTTTTCTTTCTCCTTGACCATGGTGGTCTTCCTTAT
 TGCGGTGAGTGGCAACACCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
 10 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
 ACCCAGCACTTCCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTGTC
 CTATGACCGCTATGTTGCCATCTGTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAAG
 GTGGGACTGATGATGGCTGTCTGTCATGGTTGGGGGCATCCGTGAACTCCCTAATTCACA
 15 TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA
 GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
 ATCAGCAGCATCTCCTCCTCCTCCCATCTTCTCTGATTCTACATCCTATGTCTTCATCCTT
 CAAAGTGTCACTCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
 CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
 20 TCCCAGTGCCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
 CATTGAATTCTCTGATTATATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
 GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
 TAG (SEQ ID NO: 166)

25 **AOLFR90 sequences:**

MFSMTTEALNMFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
 VLLGLSQNPVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
 CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMC DLYPLLELACTDTHIFGLMVVINS
 30 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
 AIFYIILNPLNPLYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCCTTGGATGTACCAACTTGTTAA
 TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCTTTGTCCTAATTGCAGACTATA
 35 CATGATCCCTGTTGGAGCTTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
 ACTGAGTTTGTCTCCTCTGGGACTTTACAGAATCCAAATGTTAGGAAATAGTATTTGTTG
 TATTTTTGTTTGTCTACATTGCAACTGTTGGGGCAACATGCTAATTGTAGTAACCATTTCTC
 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTCTGGA
 TGCGTGCTTCTCATCTGTCTCATCACCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
 40 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
 AGGTGATTGTCTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGTGAAGCCCTTGCA
 TTA CTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
 GGCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
 TGTCTCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
 45 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
 TTGCTTGTCTCCTATGCTGTCTCTGCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
 GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
 TATTTGTATATACAGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
 ATCATCTTAAATCCCTTGCTCAATCCTTTGATTACACTTTCAGGAATAAGGAAGTAAAC
 50 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAATATTA
 AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFVVLVVYTLTATGNITHISLIWIDHRLQTPMYFFLSNLSFL
 55 DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
 MNSRACLLVLGCWVGAFSLVLFPTIVVTRLPHYCRKEINHFFCDIAPLLQVACINTHLIEKINFL

AOLFR87 sequences:

MNNIAQLSLGFDLGPSVLQKJILTKJILLFKMYVSNCPCAIHRKINYPNTKLDFEQVNNITEFI
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLHVVTITTTSPALDSPVYFFLSFFSFIDGCSSTMAP
 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCGL
 5 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLLKLSCTDTHVFGLFVAANSGLM
 CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
 LNPLIYTLRNTTEVKNAMKQLWSQIHWGNLDCD (SEQ ID NO: 161)

10 ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
 AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
 TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACTGGATTTCGAGCAAGTGAAC
 AACATAACGGAAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
 TTGCTGTGTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATGTGGTGACA
 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTTCTGTCTTTCTTTCTTCAT
 15 AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG
 AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCT
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTG
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTCTGTGGCCC
 20 CAATGTCATTGACCATTTTCATCTGTGACCTTTCCCTCTGCTAAAACTCTCCTGCACTGACA
 CTCACGCTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
 ATTCTTATTACCTCTTACGTCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA
 25 AACCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

30 MWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGA SVNSLIHMAILMHFFPCGPRKVYHYCEFPVVKLVC
 GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRDVTQCIQRLQLWLP
 RV (SEQ ID NO: 163)

35 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
 CCCTTACCCACCTTTTCTCTCTTGACCATGGTGGTCTTCTTATTGCGGTGAGTGGC
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
 40 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTCTCTTAGCTGTCTATGCTCCTATGACCGCTAT
 GTTGCCATCTGTCTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGATGATGA
 TGGCTGTCTATGTCATGGTTGGGGGCATCCGTGAACTCCCTAATTCACATGGCGATCTTGAT
 GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCCAGCTGTTG
 45 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
 CCTCCTCCTCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCCACCTCACGGTG
 GTTCTCTTTGGTTTGGTGCCTGCATCTTCTCTACATGAGACCCAGGTCCCAGTGCATCT
 50 ATTGAGACAAGTTGGTCTGTGTTCTACAGCATCATTACGCCACATTGAATTCTCTG
 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
 GTTATACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
 164)

AOLFR89 sequences:

55 MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLIAVS
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL

ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCTCAGGGATGTGTGGGTCAGGGTT
CGAGGAGTTTTTGAAGAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCCTCCAACAAA
GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

5

AOLFR85 sequences:

MGAKNNVTEFVLFGLFESREMQHTCFVVFFLHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTLLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSISMISLASFFILIISYVILLNLRSSQSEDRRAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLILFNIVMPPLLNPLIYTLRNNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

10

ATGGGTGCCAAGAACAATGTGACTGAGTTTGTATTTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCCTCTTTCATGTGCTCACTGTCCTGGGGAACCTT
CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA
GCCAGTTGTCTTTTGTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
CTTCTTTGGTGGCACTGAGATCTTCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
ATCTGTAGGCCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCCTCCTGGTTAGCTGGCTTCTGCACTCCATCCTGCAGACCCTCCTCACGGTTGAGCTG
CCTTTTTGTGGGCCCAATGAGATAGACAACCTTCTTGTGATGTTTCATCCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
TTAGCATCCTTTTTTATCCTTATCATTTCTCTATGTTATCATCTTACTGAACCTAAGAAGCCA
GTCATCTGAGGACCGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTT
TTGGTTCTCATGCCCCCATGTTTCATGTACATTGCTCCCTCCACCACCCTGGCTGCTGACAA
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCTTTGATCTATACACTAA
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)

20

25

AOLFR86 sequences:

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNIFFMLGLSQNSEVQRVLFVFFLLIYVVTVC
GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAVLGGFLHSLVQLLLVWLWLPFC
GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYVILYSLRSHSADGRC
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

35

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
CTCAGTGACCTTGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTTGCTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGTATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCACTTATTGGTTCAG
CTCCTCCTGGTCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTGCCTGTGA
CTTGTAACCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT
GCCAACAGTGGTTTAACTGCTGCTGTTGAACTTCTCATGCTGGCTGCCTCCTACATTGTGAT
CCTGTACTCCTTGAGGTCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGTTGCTTGTCTTTGTGCCCTGTATTTTACTTATGTGCATCCATTT
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
TCCAATCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA
TGGTAA (SEQ ID NO: 160)

55

ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
TGGATTTCTGTGGCCCAATGTCAATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCCTGGCGGATGCTTTCTACG
GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
5 GGTGAAGACTGCCTGGGGGAGGAGCAAAAGCCTTCTCCACCTGCTCTTCCCACCTACCGTG
GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTTACCCTCAACCCCT
CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTCCCTTTCTTC
AGAAATTAA (SEQ ID NO: 152)

10

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKJVFVIFLRLYLGTLLGNLLIISVKASQALKNPMFFFLFYLSL
SDTCLSTSIAPRMIVDALLKKTTSFSECMIQVFSSHVFGCLEIFILILTAVDRYVDICKPLHYMTII
SQWVCGVLMVAWVWGSCVHSLVQIFLALSPLFCGPNVINHCFCDLQPLLKQACSETYVNNLL
15 VNSGAICAVSYVMLIFSIVFLHSLRNHSAEVIKKALSTCVSHIIVILFFGPCIFMYTGPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

20

ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
GGAAGAAAATAGTGTITGTTATTTTTTGCCTCTCTACTTGGGAACACTGTTGGGTAATTT
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACCTTAAGAACCCAATGTTCTTCTTCTT
TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACCTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
CATCTGTAAGCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTITTTGATG
25 GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTGAAA
CAAGCCTGTTCAAGAACCTATGTGGTTAACCTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTCATGCTAATATTCTCCTATGTCATCTTCTTGCACTTCTCTGAGAAAC
CACAGTGCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGTCA
30 TCTTGTTCTTTGGACCTTGCAATTTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT
AAGATGATAGCTGTATTTTATACAGTTTGAACATCTTTCTCAACCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

35

AOLFR83 sequences:

MGNWTAAVTEFVLLGFSLSREVELLLLVLPTFLLTLLGNLLIISTVLSCSRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMYSYDRYATICPLRYT
TIMRPSVCIGTVVFSWVGGLSVLFPTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
MLSSMVLCCIVLVAYSYTYIILTVRIPSASGRKKAFTNCASHLTIVIPSGITVFIYVTPSQKEYL
40 EINKIPLVLSSVTPFLNPFIYTLRNDTVQGVLRDVWVRVGRGVFEKRMRAVLRSLSSNKDHO
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

45

ATGGGTAAGTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACAGTTCCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGTCTGCTCCCGCCTCCACACCCCATGTACTTCTTCT
TGTGCAACCTCTCTATCCTGGACATCCTCTTCACCTCAGTCATCTCTCCAAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT
ACTTTTTCTTGGGCACAGTTGAGTTCCTCCTGCTGACGGTCACTGTCCTATGACCGTTATGCC
ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG
50 TTGTATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTCCAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAAACCACTTCTTCTGTGACAGTGGACCTTGTGGC
CCTGGCCTGTGCAGACCACTGCCATCGAGCTGATGGATTTATGCTTTCTTCCATGGTC
ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTTATACGTACATCATCTTGACCATAGTGCG
CATTCCTTCTGCAAGTGGAAGGAAGAAGGCCTTAATACCTGTGCTTCCCACCTGACCATA
55 GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCTCAACCCCTTT

CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
 CTCCAAAGCCCAATGTATTTCTTCCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT
 GTGGTCACACCTAAGCTCTTGGTCAACTTCCTGGTCTCTGACAAGTCCATCTCTTTTGAGG
 GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCCTGCTGGC
 5 CTCCATGGCCTATGACCGCTTCCTAGCCATCTGTCAACCCCTCCATTATGGTTCATCATGA
 CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTTGGTGGAGCCAACTCCGC
 TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCCAACCAAGCTAACACACTAC
 TACTGTGACATACCACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
 TCCTCTATGTCTTTCTGCTCTGGTCACCCCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT
 10 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
 CCCTTGTGCCTCCCACCTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTCACCTAT
 GTTCAGCCCCATGGATCTACTAACAAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA
 TCATAATTCCCATGCTCAATCCCTTCATCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

15

AOLFR80 sequences:

MEGINKTAKMQFFRPFSPDPEVQMLIFVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
 PLRYRLMSWSLCEVLLVGSLLVGLSLPLTILIFHLFPCHNDEIYHFYCDMPAVMRLACADTR
 20 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYILSPS
 SSSPEMGRVVSVAYTFITPILNPLIYSLRNKELKDALKALRK (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTTTCTTTCTCGTCCATTCTCACCTGACC
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGTATCTGACCAGCCTCGGTGG
 25 AAATGGCTACAATTGCAGTCATTGTTTCAGATCAATCATTCCCTCCACACCCCCATGTACTTTT
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTTGGCCTTG
 GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
 TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCCTGCTGGTAGTCATGGCTTATGACCGG
 TTTATAGCGATCTGTACCCCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGTGG
 30 AGCTGCTGGTAGGCTCCTTGGTGTGCTGGGGTTCTGTTGTCACTGCCACTCACCATTTAATC
 TTCCATCTCCCATTCTGCCACAATGATGAGATCTACCATTCTACTGTGACATGCCTGCAGT
 CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
 TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
 35 TTAGTGGTCTCCTCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTTCAGCTA
 CTCCTCTGAGATGGGCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
 CCTTGATCTATAGTTTGAGGAACAAGGAAGTGAAGATGCCCTAAGGAAAGCATTGAGA
 AAATTCTAG (SEQ ID NO: 150)

40 **AOLFR81 sequences:**

MGVKNHSTVTEFLLSGLTEQAELQLPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
 LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSRMMSNQTLVTEFILQGFSEHPEYRVFLFSCF
 LFLYSGALTGNVILITLITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC
 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
 45 TGLMLRLDFCGPNVHHFFCEVPPLLLSCSSSTYVNGVMIVLADAFYGIVNFMFTIASYGFIVSSI
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
 IYTLRNKEVKAALRKLFPFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCAGAAACCCGTCCCAGCCCAAGGATG
 50 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTTCGGAGCACCAGAAAT
 ACCGGGTGTTCTTATTCAGCTGTTTCTCTCTACTCTGGGGCCCTCACAGGTAATGTC
 CTCATCACCTTGGCCATCACGTTCAACCCCTGGGCTCCACGCTCCTATGTACTTTTTCTTACT
 CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT
 CTGGTGTGCGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTCTATTCTCA
 55 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC